

## SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD.

<120> Shear stress-responsive genes

<130> PH-1064-PCT

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<150> JP 1999-280976

<151> 1999-10-01

<160> 181

<170> PatentIn Ver. 2.0

<210> 1

<211> 3817

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (440).. (1930)

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Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr

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gac tat gac ctt atc atc att gga ggt ggc tca gga ggt ctg gca gct			520
Asp Tyr Asp Leu Ile Ile Ile Gly Gly Gly Ser Gly Gly Leu Ala Ala			
15	20	25	
gct aag gag gca gcc caa tat ggc aag aag gtg atg gtc ctg gac ttt			568
Ala Lys Glu Ala Ala Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe			
30	35	40	
gtc act ccc acc cct ctt gga act aga tgg ggt ctt gga gga aca tgt			616
Val Thr Pro Thr Pro Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys			
45	50	55	
gtg aat gtg ggt tgc ata cct aaa aaa ctg atg cat caa gca gct ttg			664
Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu			
60	65	70	75
tta gga caa gcc ctg caa gac tct cga aat tat gga tgg aaa gtc gag			712
Leu Gly Gln Ala Leu Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu			
80	85	90	
gag aca gtt aag cat gat tgg gac aga atg ata gaa gct gta cag aat			760
Glu Thr Val Lys His Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn			
95	100	105	
cac att ggc tct ttg aat tgg ggc tac cga gta gct ctg cgg gag aaa			808
His Ile Gly Ser Leu Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys			
110	115	120	
aaa gtc gtc tat gag aat gct tat ggg caa ttt att ggt cct cac agg			856
Lys Val Val Tyr Glu Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg			
125	130	135	
att aag gca aca aat aat aaa ggc aaa gaa aaa att tat tca gca gag			904

Ile Lys Ala Thr Asn Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu	
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agt ttt ctc att gcc act ggt gaa aga cca cgt tac ttg ggc atc cct	952
Ser Phe Leu Ile Ala Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro	
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Gly Asp Lys Glu Tyr Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro	
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Tyr Cys Pro Gly Lys Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu	
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Val Arg Ser Ile Leu Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys	
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att ggt gaa cac atg gaa gaa cat ggc atc aag ttt ata aga cag ttc	1192
Ile Gly Glu His Met Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe	
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gta cca att aaa gtt gaa caa att gaa gca ggg aca cca ggc cga ctc	1240
Val Pro Ile Lys Val Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu	
255	260
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aga gta gta gct cag tcc acc aat agt gag gaa atc att gaa gga gaa	1288
Arg Val Val Ala Gln Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu	
270	275
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Tyr Asn Thr Val Met Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys	
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Ile Gly Leu Glu Thr Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys	
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Ile Gly Asp Ile Leu Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile	
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Gln Ala Gly Arg Leu Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val	
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Lys Cys Asp Tyr Glu Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu	
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Tyr Gly Ala Cys Gly Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly	
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Glu Glu Asn Ile Glu Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp	
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Thr Ile Pro Ser Arg Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys	
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Asn Thr Lys Asp Asn Glu Arg Val Val Gly Phe His Val Leu Gly Pro

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455

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Leu Thr Lys Lys Gln Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys

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485

490

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Ile Leu Gln Ala Gly Cys

495

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<210> 2

<211> 497

<212> PRT

<213> Homo sapiens

<400> 2

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Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys			
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Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gln Ala Leu			
65	70	75	80
Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu Thr Val Lys His			
85	90	95	
Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His Ile Gly Ser Leu			
100	105	110	
Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys Val Val Tyr Glu			
115	120	125	
Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile Lys Ala Thr Asn			
130	135	140	
Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Ser Phe Leu Ile Ala			
145	150	155	160
Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly Asp Lys Glu Tyr			
165	170	175	
Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr Cys Pro Gly Lys			
180	185	190	
Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe			
195	200	205	
Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met Val Arg Ser Ile Leu			
210	215	220	

Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile Gly Glu His Met			
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Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val			
245	250	255	
Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln			
260	265	270	
Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr Asn Thr Val Met			
275	280	285	
Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile Gly Leu Glu Thr			
290	295	300	
Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile Pro Val Thr Asp			
305	310	315	320
Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu			
325	330	335	
Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu			
340	345	350	
Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu			
355	360	365	
Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly			
370	375	380	
Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu			
385	390	395	400
Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg			
405	410	415	
Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn Thr Lys Asp Asn			
420	425	430	

Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val

435

440

445

Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu Thr Lys Lys Gln

450

455

460

Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr

465

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480

Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile Leu Gln Ala Gly

485

490

495

Cys

<210> 3

<211> 1487

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6).. (938)

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15

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Trp Pro Arg Pro Pro Ala Pro Gly Pro Pro Pro Pro Pro Leu Pro Leu

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25

30

ctg ctc ctg ctc ctg gcc ggg ctg ctg ggc ggc gcg ggc gcg cag tac 146

Leu Leu Leu Leu Leu Ala Gly Leu Leu Gly Gly Ala Gly Ala Gln Tyr

35

40

45

tcc agc gac cgg tgc agc tgg aag ggg agc ggg ctg acg cac gag gca	194
Ser Ser Asp Arg Cys Ser Trp Lys Gly Ser Gly Leu Thr His Glu Ala	
50 55 60	
cac agg aag gag gig gag cag gtg tat ctg cgc tgt gcg gcg ggt gcc	242
His Arg Lys Glu Val Glu Gln Val Tyr Leu Arg Cys Ala Ala Gly Ala	
65 70 75	
gtg gag tgg atg tac cca aca ggt gct ctc atc gtt aac ctg cgg ccc	290
Val Glu Trp Met Tyr Pro Thr Gly Ala Leu Ile Val Asn Leu Arg Pro	
80 85 90 95	
aac acc ttc tcg cct gcc cgg cac ctg acc gtg tgc atc agg tcc ttc	338
Asn Thr Phe Ser Pro Ala Arg His Leu Thr Val Cys Ile Arg Ser Phe	
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acg gac tcc tcg ggg gcc aat att tat ttg gaa aaa act gga gaa ctg	386
Thr Asp Ser Ser Gly Ala Asn Ile Tyr Leu Glu Lys Thr Gly Glu Leu	
115 120 125	
aga ctg ctg gta ccg gac ggg gac ggc agg ccc ggc cgg gtg cag tgt	434
Arg Leu Leu Val Pro Asp Gly Asp Gly Arg Pro Gly Arg Val Gln Cys	
130 135 140	
ttt ggc ctg gag cag ggc ggc ctg ttc gtg gag gcc acg ccg cag cag	482
Phe Gly Leu Glu Gln Gly Gly Leu Phe Val Glu Ala Thr Pro Gln Gln	
145 150 155	
gat atc ggc cgg agg acc aca ggc ttc cag tac gag ctg gtt agg agg	530
Asp Ile Gly Arg Arg Thr Thr Gly Phe Gln Tyr Glu Leu Val Arg Arg	
160 165 170 175	
cac agg gcg tcg gac ctg cac gag ctg tct gcg ccg tgc cgt ccc tgc	578
His Arg Ala Ser Asp Leu His Glu Leu Ser Ala Pro Cys Arg Pro Cys	
180 185 190	

agt gac acc gag gtg ctc cta gcc gtc tgc acc agc gac ttc gcc gtt 626  
 Ser Asp Thr Glu Val Leu Leu Ala Val Cys Thr Ser Asp Phe Ala Val  
 195 200 205  
 cga ggc tcc atc cag caa gtt acc cac gag cct gag cgg cag gac tca 674  
 Arg Gly Ser Ile Gln Gln Val Thr His Glu Pro Glu Arg Gln Asp Ser  
 210 215 220  
 gcc atc cac ctg cgc gtg agc aga ctc tat cgg cag aaa agc agg gtc 722  
 Ala Ile His Leu Arg Val Ser Arg Leu Tyr Arg Gln Lys Ser Arg Val  
 225 230 235  
 ttc gag ccg gtg ccc gag ggt gac ggc cac tgg cag ggg cgc gtc agg 770  
 Phe Glu Pro Val Pro Glu Gly Asp Gly His Trp Gln Gly Arg Val Arg  
 240 245 250 255  
 acg ctg ctg gag tgt ggc gtg cgg ccg ggg cat ggc gac ttc ctc ttc 818  
 Thr Leu Leu Glu Cys Gly Val Arg Pro Gly His Gly Asp Phe Leu Phe  
 260 265 270  
 act ggc cac atg cac ttc ggg gag gcg cgg ctc ggc tgt gcc cca cgc 866  
 Thr Gly His Met His Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro Arg  
 275 280 285  
 ttc aag gac ttc cag agg atg tac agg gat gcc cag gag agg ggg ctg 914  
 Phe Lys Asp Phe Gln Arg Met Tyr Arg Asp Ala Gln Glu Arg Gly Leu  
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 aac cct tgt gag gtt ggc acg gac tgactccgtg ggccgctgcc ctctctctcc 968  
 Asn Pro Cys Glu Val Gly Thr Asp  
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<211> 311

<212> PRT

<213> Homo sapiens

<400> 4

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Leu	Leu	Leu	Leu	Ala	Gly	Leu	Leu	Gly	Gly	Ala	Gly	Ala	Gln	Tyr	Ser
				35				40					45		
Ser	Asp	Arg	Cys	Ser	Trp	Lys	Gly	Ser	Gly	Leu	Thr	His	Glu	Ala	His
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Arg	Lys	Glu	Val	Glu	Gln	Val	Tyr	Leu	Arg	Cys	Ala	Ala	Gly	Ala	Val
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Glu	Trp	Met	Tyr	Pro	Thr	Gly	Ala	Leu	Ile	Val	Asn	Leu	Arg	Pro	Asn
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Thr	Phe	Ser	Pro	Ala	Arg	His	Leu	Thr	Val	Cys	Ile	Arg	Ser	Phe	Thr
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Asp Ser Ser Gly Ala Asn Ile Tyr Leu Glu Lys Thr Gly Glu Leu Arg			
115	120	125	
Leu Leu Val Pro Asp Gly Asp Gly Arg Pro Gly Arg Val Gln Cys Phe			
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Gly Leu Glu Gln Gly Gly Leu Phe Val Glu Ala Thr Pro Gln Gln Asp			
145	150	155	160
Ile Gly Arg Arg Thr Thr Gly Phe Gln Tyr Glu Leu Val Arg Arg His			
165	170	175	
Arg Ala Ser Asp Leu His Glu Leu Ser Ala Pro Cys Arg Pro Cys Ser			
180	185	190	
Asp Thr Glu Val Leu Leu Ala Val Cys Thr Ser Asp Phe Ala Val Arg			
195	200	205	
Gly Ser Ile Gln Gln Val Thr His Glu Pro Glu Arg Gln Asp Ser Ala			
210	215	220	
Ile His Leu Arg Val Ser Arg Leu Tyr Arg Gln Lys Ser Arg Val Phe			
225	230	235	240
Glu Pro Val Pro Glu Gly Asp Gly His Trp Gln Gly Arg Val Arg Thr			
245	250	255	
Leu Leu Glu Cys Gly Val Arg Pro Gly His Gly Asp Phe Leu Phe Thr			
260	265	270	
Gly His Met His Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro Arg Phe			
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49).. (2664)

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Gly Ala Ala Gln Glu Leu Gln Ala Lys Leu Ala Glu Ile Gly Ala Pro

5

10

15

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Ile Gln Gly Asn Arg Glu Glu Leu Val Glu Arg Leu Gln Ser Tyr Thr

20

25

30

35

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Arg Gln Thr Gly Ile Val Leu Asn Arg Pro Val Leu Arg Gly Glu Asp

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Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu Pro Gly Ile

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65

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Pro Met Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln Pro Pro Pro

70

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His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val Gly Glu Pro	
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Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val Arg Thr Pro	
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Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro Ser Val Gly	
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Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu Lys Glu Ser	
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Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Glu Met Glu Thr	
260 265 270 275	
gat gct cgc tcg tcc ctg ggc cag tca gcg tca gag act gag gag gac	921
Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr Glu Glu Asp	
280 285 290	
aca gig tcc gta tct aaa aag gag aaa aac cgg aag cgt agg aac cga	969
Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg Arg Asn Arg	
295 300 305	
aag aag aag aaa aag ccc cag cgg gtg cga ggg gtg tcc tct gag agc	1017
Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser Ser Glu Ser	
310 315 320	
tct ggg gac cgg gag aaa gac tca acc cgg tcc cgt ggc tct gat tcc	1065
Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly Ser Asp Ser	
325 330 335	
cca gca gct gat gtt gag att gag tat gtg act gaa gaa cct gaa att	1113
Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu Pro Glu Ile	
340 345 350 355	
tac gag ccc aac ttt atc ttc ttt aag agg atc ttt gag gct ttt aag	1161
Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu Ala Phe Lys	
360 365 370	

ctc act gat gat gtg aag aag gag aaa gag aaa gag cca gag aaa ctt	1209
Leu Thr Asp Asp Val Lys Lys Glu Lys Glu Lys Glu Pro Glu Lys Leu	
375 380 385	
gac aaa ctg gag aac tct gca gcc ccc aag aag aag gga ttt gaa gag	1257
Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly Phe Glu Glu	
390 395 400	
gag cac aag gac agt gat gat gac agc agt gat gac gag cag gaa aag	1305
Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu Gln Glu Lys	
405 410 415	
aag cca gaa gcc ccc aag ctg tcc aag aag aag ttg cgc cga atg aac	1353
Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg Arg Met Asn	
420 425 430 435	
cgc ttc act gtg gct gaa ctc aag cag ctg gtg gct cgg ccc gat gtc	1401
Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg Pro Asp Val	
440 445 450	
gtg gag atg cac gat gtg aca gcg cag gac cct aag ctc ttg gtt cac	1449
Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu Leu Val His	
455 460 465	
ctc aag gcc act cgg aac tct gtg cct gtg cca cgc cac tgg tgt ttt	1497
Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His Trp Cys Phe	
470 475 480	
aag cgc aaa tac ctg cag ggc aaa cgg ggc att gag aag ccc ccc ttc	1545
Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys Pro Pro Phe	
485 490 495	
gag ctg cca gac ttc atc aaa cgc aca ggc atc cag gag atg cga gag	1593
Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu Met Arg Glu	

500	505	510	515	
gcc ctg cag gag aag gaa gaa cag aag acc atg aag tca aaa atg cga				1641
Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser Lys Met Arg				
	520	525	530	
gag aaa gtt cgg cct aag atg ggc aaa att gac atc gac tac cag aaa				1689
Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp Tyr Gln Lys				
	535	540	545	
ctg cat gat gcc ttc ttc aag tgg cag acc aag cca aag ctg acc atc				1737
Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys Leu Thr Ile				
	550	555	560	
cat ggg gac ctg tac tat gag ggg aag gag ttc gag aca cga ctg aag				1785
His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr Arg Leu Lys				
	565	570	575	
gag aag aag cca gga gat ctg tct gat gag cta agg att tcc ttg ggg				1833
Glu Lys Lys Pro Gly Asp Leu Ser Asp Glu Leu Arg Ile Ser Leu Gly				
580	585	590	595	
atg cca gta gga cca aat gcc cac aag gtc cct ccc cca tgg ctg att				1881
Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro Trp Leu Ile				
	600	605	610	
gcc atg cag cga tat gga cca ccc cca tcg tat ccc aac ctg aaa atc				1929
Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn Leu Lys Ile				
	615	620	625	
cct ggg ctg aac tcg ccc atc cct gag agc tgt tcc ttt ggg tac cat				1977
Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe Gly Tyr His				
	630	635	640	
gct ggt ggc tgg ggc aaa cct cca gtg gat gag act ggg aaa ccg ctc				2025
Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly Lys Pro Leu				

645	650	655	
tat ggg gac gtg ttt gga acc aat gct gct gaa ttt cag acc aag act	2073		
Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln Thr Lys Thr			
660	665	670	675
gag gaa gaa gag att gat cgg acc cct tgg ggg gaa ctg gaa cca tct	2121		
Glu Glu Glu Glu Ile Asp Arg Thr Pro Trp Gly Glu Leu Glu Pro Ser			
680	685	690	
gat gaa gaa tcc tca gaa gaa gag gaa gag gaa gaa agt gat gaa gac	2169		
Asp Glu Glu Ser Ser Glu Glu Glu Glu Glu Glu Glu Ser Asp Glu Asp			
695	700	705	
aaa cca gat gag aca ggc ttt att acc cct gca gac agt ggc ctt atc	2217		
Lys Pro Asp Glu Thr Gly Phe Ile Thr Pro Ala Asp Ser Gly Leu Ile			
710	715	720	
act cct gga ggc ttt tca tca gtg cct gct gga atg gag acc cct gaa	2265		
Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu Thr Pro Glu			
725	730	735	
ctc att gag ctg agg aag aag aag att gag gag gcg atg gac gga agt	2313		
Leu Ile Glu Leu Arg Lys Lys Lys Ile Glu Glu Ala Met Asp Gly Ser			
740	745	750	755
gag aca cct cag ctc ttc act gtg ttg cca gag aag aga aca gcc act	2361		
Glu Thr Pro Gln Leu Phe Thr Val Leu Pro Glu Lys Arg Thr Ala Thr			
760	765	770	
ggt gga ggg gcc atg atg gga tca acc cac att tat gac atg tcc acg	2409		
Val Gly Gly Ala Met Met Gly Ser Thr His Ile Tyr Asp Met Ser Thr			
775	780	785	
ggt atg agc cgg aag ggc ccg gct cct gag ctg caa ggt gtg gaa gtg	2457		

Val Met Ser Arg Lys Gly Pro Ala Pro Glu Leu Gln Gly Val Glu Val  
790 795 800  
gcg ctg gcg cct gaa gag ttg gag ctg gat cct atg gcc atg acc cag 2505  
Ala Leu Ala Pro Glu Glu Leu Glu Leu Asp Pro Met Ala Met Thr Gln  
805 810 815  
aag tat gag gag cat gtg cgg gag cag cag gct caa gta gag aag gag 2553  
Lys Tyr Glu Glu His Val Arg Glu Gln Gln Ala Gln Val Glu Lys Glu  
820 825 830 835  
gac ttc agt gac atg gtg gct gag cac gct gcc aaa cag aag caa aaa 2601  
Asp Phe Ser Asp Met Val Ala Glu His Ala Ala Lys Gln Lys Gln Lys  
840 845 850  
aaa cgg aaa gct cag ccc cag gac agc cgt ggg ggc agc aag aaa tat 2649  
Lys Arg Lys Ala Gln Pro Gln Asp Ser Arg Gly Gly Ser Lys Lys Tyr  
855 860 865  
aag gag ttc aag ttt taggtcccct cacactagcc ctttttttgg ccctacgtct 2704  
Lys Glu Phe Lys Phe  
870  
ggatgcctgg gcttcacaca agaaccacct ctcccgagct tccaaggac ttgtcatttc 2764  
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 Ser Tyr Thr Arg Gln Thr Gly Ile Val Leu Asn Arg Pro Val Leu Arg  
                   35                                  40                                  45  
 Gly Glu Asp Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu  
                   50                                  55                                  60  
 Pro Gly Ile Pro Met Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln  
                   65                                  70                                  75                                  80  
 Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Leu Gly Leu Gly Phe  
                                   85                                  90                                  95  
 Pro Met Ala His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val  
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 Gly Glu Pro Val Ala Leu Ser Glu Glu Glu Arg Leu Lys Leu Ala Gln  
                   115                                  120                                  125  
 Gln Gln Ala Ala Leu Leu Met Gln Gln Glu Glu Arg Ala Lys Gln Gln  
                   130                                  135                                  140  
 Gly Asp His Ser Leu Lys Glu His Glu Leu Leu Glu Gln Gln Lys Arg  
                   145                                  150                                  155                                  160  
 Ala Ala Val Leu Leu Glu Gln Glu Arg Gln Gln Glu Ile Ala Lys Met  
                                   165                                  170                                  175  
 Gly Thr Pro Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val  
                   180                                  185                                  190  
 Arg Thr Pro Leu Gly Pro Arg Val Ala Ala Pro Val Gly Pro Val Gly  
                   195                                  200                                  205  
 Pro Thr Pro Thr Val Leu Pro Met Gly Ala Pro Val Pro Arg Pro Arg  
                   210                                  215                                  220  
 Gly Pro Pro Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro

225	230	235	240
Ser Val Gly Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu			
	245	250	255
Lys Glu Ser Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Glu			
	260	265	270
Met Glu Thr Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr			
	275	280	285
Glu Glu Asp Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg			
	290	295	300
Arg Asn Arg Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser			
305	310	315	320
Ser Glu Ser Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly			
	325	330	335
Ser Asp Ser Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu			
	340	345	350
Pro Glu Ile Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu			
	355	360	365
Ala Phe Lys Leu Thr Asp Asp Val Lys Lys Glu Lys Glu Lys Glu Pro			
	370	375	380
Glu Lys Leu Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly			
385	390	395	400
Phe Glu Glu Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu			
	405	410	415
Gln Glu Lys Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg			
	420	425	430
Arg Met Asn Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg			

435	440	445	
Pro Asp Val Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu			
450	455	460	
Leu Val His Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His			
465	470	475	480
Trp Cys Phe Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys			
	485	490	495
Pro Pro Phe Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu			
	500	505	510
Met Arg Glu Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser			
	515	520	525
Lys Met Arg Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp			
	530	535	540
Tyr Gln Lys Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys			
545	550	555	560
Leu Thr Ile His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr			
	565	570	575
Arg Leu Lys Glu Lys Lys Pro Gly Asp Leu Ser Asp Glu Leu Arg Ile			
	580	585	590
Ser Leu Gly Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro			
	595	600	605
Trp Leu Ile Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn			
	610	615	620
Leu Lys Ile Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe			
625	630	635	640
Gly Tyr His Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly			
	645	650	655



Lys Lys Tyr Lys Glu Phe Lys Phe

865

870

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<211> 2433

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (214).. (1146)

<400> 7

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ctggctccccg gaggtctctg ccagctcgac agtgttcttg gcacigctca aaggctccag 180  
cagctggggt tccccgtcag cccgtgagcg gcc atg tcc aac ccc agc gcc cca 234

Met Ser Asn Pro Ser Ala Pro

1

5

cca cca tat gaa gac cgc aac ccc ctg tac cca ggc cct ccg ccc cct 282

Pro Pro Tyr Glu Asp Arg Asn Pro Leu Tyr Pro Gly Pro Pro Pro Pro

10

15

20

ggg ggc tat ggg cag cca tct gtc ctg cca gga ggg tat cct gcc tac 330

Gly Gly Tyr Gly Gln Pro Ser Val Leu Pro Gly Gly Tyr Pro Ala Tyr

25

30

35

cct ggc tac ccg cag cct ggc tac ggt cac cct gct ggc tac cca cag 378

Pro Gly Tyr Pro Gln Pro Gly Tyr Gly His Pro Ala Gly Tyr Pro Gln

40

45

50

55

ccc atg ccc ccc acc cac ccg atg ccc atg aac tac ggc cca ggc cat 426

Pro Met Pro Pro Thr His Pro Met Pro Met Asn Tyr Gly Pro Gly His	
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ggc tat gat ggg gag gag aga gcg gtg agt gat agc ttc ggg cct gga	474
Gly Tyr Asp Gly Glu Glu Arg Ala Val Ser Asp Ser Phe Gly Pro Gly	
75 80 85	
gag tgg gat gac cgg aaa gtg cga cac act ttt atc cga aag gtt tac	522
Glu Trp Asp Asp Arg Lys Val Arg His Thr Phe Ile Arg Lys Val Tyr	
90 95 100	
tcc atc atc tcc gtg cag ctg ctc atc act gtg gcc atc att gct atc	570
Ser Ile Ile Ser Val Gln Leu Leu Ile Thr Val Ala Ile Ile Ala Ile	
105 110 115	
ttc acc ttt gtg gaa cct gtc agc gcc ttt gtg agg aga aat gtg gct	618
Phe Thr Phe Val Glu Pro Val Ser Ala Phe Val Arg Arg Asn Val Ala	
120 125 130 135	
gtc tac tac gtg tcc tat gct gtc ttc gtt gtc acc tac ctg atc ctt	666
Val Tyr Tyr Val Ser Tyr Ala Val Phe Val Val Thr Tyr Leu Ile Leu	
140 145 150	
gcc tgc tgc cag gga ccc aga cgc cgt ttc cca tgg aac atc att ctg	714
Ala Cys Cys Gln Gly Pro Arg Arg Arg Phe Pro Trp Asn Ile Ile Leu	
155 160 165	
ctg acc ctt ttt act ttt gcc atg ggc ttc atg acg ggc acc att tcc	762
Leu Thr Leu Phe Thr Phe Ala Met Gly Phe Met Thr Gly Thr Ile Ser	
170 175 180	
agt atg tac caa acc aaa gcc gtc atc att gca atg atc atc act gcg	810
Ser Met Tyr Gln Thr Lys Ala Val Ile Ile Ala Met Ile Ile Thr Ala	
185 190 195	
gtg gla tcc att tca gtc acc atc ttc tgc ttt cag acc aag gtg gac	858

Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe Gln Thr Lys Val Asp  
200 205 210 215  
ttc acc tgc tgc aca ggc ctc ttc tgt gtc ctg gga att gtg ctc ctg 906  
Phe Thr Ser Cys Thr Gly Leu Phe Cys Val Leu Gly Ile Val Leu Leu  
220 225 230  
gtg act ggg att gtc act agc att gtg ctc tac ttc caa tac gtt tac 954  
Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr  
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Trp Leu His Met Leu Tyr Ala Ala Leu Gly Ala Ile Cys Phe Thr Leu  
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ttc ctg gct tac gac aca cag ctg gtc ctg ggg aac cgg aag cac acc 1050  
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<211> 311

<212> PRT

<213> Homo sapiens

<400> 8

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Tyr Pro Gly Pro Pro Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu

20 25 30

Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly



35	40	45
His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro		
50	55	60
Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val		
65	70	75
Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His		
85	90	95
Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu Ile		
100	105	110
Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser Ala		
115	120	125
Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe		
130	135	140
Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg		
145	150	155
Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly		
165	170	175
Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile		
180	185	190
Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe		
195	200	205
Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys		
210	215	220
Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val		
225	230	235
Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu		
245	250	255

Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val

260

265

270

Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly

275

280

285

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<213> Homo sapiens

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Met Pro Glu Lys Arg Pro Phe Glu Arg

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ctg cct gcc gat gtc tcc ccc atc aac tac agc ctt tgc ctc aag ccc 160

Leu Pro Ala Asp Val Ser Pro Ile Asn Tyr Ser Leu Cys Leu Lys Pro

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15

20

25

gac ttg ctg gac ttc acc ttc gag ggc aag ctg gag gcc gcc gcc cag 208

Asp Leu Leu Asp Phe Thr Phe Glu Gly Lys Leu Glu Ala Ala Ala Gln

30

35

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att att aca gct tca tat gca cca gaa gga gat gaa gaa ata cat gct	304
Ile Ile Thr Ala Ser Tyr Ala Pro Glu Gly Asp Glu Glu Ile His Ala	
60 65 70	
aca gga ttt aac tat cag aat gaa gat gaa aaa gtc acc ttg tct ttc	352
Thr Gly Phe Asn Tyr Gln Asn Glu Asp Glu Lys Val Thr Leu Ser Phe	
75 80 85	
cct agt act ctg caa aca ggt acg gga acc tta aag ata gat ttt gtt	400
Pro Ser Thr Leu Gln Thr Gly Thr Gly Thr Leu Lys Ile Asp Phe Val	
90 95 100 105	
gga gag ctg aat gac aaa atg aaa ggt ttc tat aga agt aaa tat act	448
Gly Glu Leu Asn Asp Lys Met Lys Gly Phe Tyr Arg Ser Lys Tyr Thr	
110 115 120	
acc cct tct gga gag gtg cgc tat gct gct gta aca cag ttt gag gct	496
Thr Pro Ser Gly Glu Val Arg Tyr Ala Ala Val Thr Gln Phe Glu Ala	
125 130 135	
act gat gcc cga agg gct ttt cct tgc tgg gat gag cct gct atc aaa	544
Thr Asp Ala Arg Arg Ala Phe Pro Cys Trp Asp Glu Pro Ala Ile Lys	
140 145 150	
gca act ttt gat atc tca ttg gtt gtt cct aaa gac aga gta gct tta	592
Ala Thr Phe Asp Ile Ser Leu Val Val Pro Lys Asp Arg Val Ala Leu	
155 160 165	
tca aac atg aat gta att gac cgg aaa cca tac cct gat gat gaa aat	640
Ser Asn Met Asn Val Ile Asp Arg Lys Pro Tyr Pro Asp Asp Glu Asn	

170	175	180	185	
tta gtg gaa gtg aag ttt gcc cgc aca cct gtt atg tct aca tat ctg	688			
Leu Val Glu Val Lys Phe Ala Arg Thr Pro Val Met Ser Thr Tyr Leu				
190	195	200		
gig gca ttt gtt gtg ggt gaa tat gac ttt gta gaa aca agg tca aaa	736			
Val Ala Phe Val Val Gly Glu Tyr Asp Phe Val Glu Thr Arg Ser Lys				
205	210	215		
gat ggt gtg tgt gtc cgt gtt tac act cct gtt ggc aaa gca gag caa	784			
Asp Gly Val Cys Val Arg Val Tyr Thr Pro Val Gly Lys Ala Glu Gln				
220	225	230		
gga aaa ttt gcg tta gag gtt gct gct aaa acc ttg cct ttt tat aag	832			
Gly Lys Phe Ala Leu Glu Val Ala Ala Lys Thr Leu Pro Phe Tyr Lys				
235	240	245		
gac tac ttc aat gtt cct tat cct cta cct aaa att gat ctc att gct	880			
Asp Tyr Phe Asn Val Pro Tyr Pro Leu Pro Lys Ile Asp Leu Ile Ala				
250	255	260	265	
att gca gac ttt gca gct ggt gcc atg gag aac tgg ggc ctt gtt act	928			
Ile Ala Asp Phe Ala Ala Gly Ala Met Glu Asn Trp Gly Leu Val Thr				
270	275	280		
tat agg gag act gca ttg ctt att gat cca aaa aat tcc tgt tct tca	976			
Tyr Arg Glu Thr Ala Leu Leu Ile Asp Pro Lys Asn Ser Cys Ser Ser				
285	290	295		
tcc cgc cag tgg gtt gct ctg gtt gtg gga cat gaa ctc gcc cat caa	1024			
Ser Arg Gln Trp Val Ala Leu Val Val Gly His Glu Leu Ala His Gln				
300	305	310		
tgg ttt gga aat ctt gtt act atg gaa tgg tgg act cat ctt tgg tta	1072			
Trp Phe Gly Asn Leu Val Thr Met Glu Trp Trp Thr His Leu Trp Leu				

315	320	325	
aat gaa ggt ttt gca tcc tgg att gaa tat ctg tgt gta gac cac tgc	1120		
Asn Glu Gly Phe Ala Ser Trp Ile Glu Tyr Leu Cys Val Asp His Cys			
330	335	340	345
ttc cca gag tat gat att tgg act cag ttt gtt tct gct gat tac acc	1168		
Phe Pro Glu Tyr Asp Ile Trp Thr Gln Phe Val Ser Ala Asp Tyr Thr			
350	355	360	
cgt gcc cag gag ctt gac gcc tta gat aac agc cat cct att gaa gtc	1216		
Arg Ala Gln Glu Leu Asp Ala Leu Asp Asn Ser His Pro Ile Glu Val			
365	370	375	
agt gtg ggc cat cca tct gag gtt gat gag ata ttt gat gct ata tca	1264		
Ser Val Gly His Pro Ser Glu Val Asp Glu Ile Phe Asp Ala Ile Ser			
380	385	390	
tat agc aaa ggt gca tct gtc atc cga atg ctg cat gac tac att ggg	1312		
Tyr Ser Lys Gly Ala Ser Val Ile Arg Met Leu His Asp Tyr Ile Gly			
395	400	405	
gat aag gac ttt aag aaa gga atg aac atg tat tta acc aag ttc caa	1360		
Asp Lys Asp Phe Lys Lys Gly Met Asn Met Tyr Leu Thr Lys Phe Gln			
410	415	420	425
caa aag aat gct gcc aca gag gat ctc tgg gaa agt tta gaa aat gct	1408		
Gln Lys Asn Ala Ala Thr Glu Asp Leu Trp Glu Ser Leu Glu Asn Ala			
430	435	440	
agt ggt aaa cct ata gca gct gtg atg aat acc tgg acc aaa caa atg	1456		
Ser Gly Lys Pro Ile Ala Ala Val Met Asn Thr Trp Thr Lys Gln Met			
445	450	455	
gga ttt ccc ctc att tat gtg gaa gct gaa cag gta gaa gat gac aga	1504		

Gly Phe Pro Leu Ile Tyr Val Glu Ala Glu Gln Val Glu Asp Asp Arg	
460	465
470	
tta ttg agg ttg tcc caa aag aag ttc tgt gct ggt ggg tca tat gtt	1552
Leu Leu Arg Leu Ser Gln Lys Lys Phe Cys Ala Gly Gly Ser Tyr Val	
475	480
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ggt gaa gat tgt ccc cag tgg atg gtc cct atc aca atc tct act agt	1600
Gly Glu Asp Cys Pro Gln Trp Met Val Pro Ile Thr Ile Ser Thr Ser	
490	495
500	505
gaa gac ccc aac cag gcc aaa cta aaa att cta atg gac aag cca gag	1648
Glu Asp Pro Asn Gln Ala Lys Leu Lys Ile Leu Met Asp Lys Pro Glu	
510	515
520	
atg aat gtg gtt ttg aaa aat gtc aaa cca gac caa tgg gtg aag tta	1696
Met Asn Val Val Leu Lys Asn Val Lys Pro Asp Gln Trp Val Lys Leu	
525	530
535	
aac tta gga aca gtt ggg ttt tat cgg acc cag tac agc tct gcc atg	1744
Asn Leu Gly Thr Val Gly Phe Tyr Arg Thr Gln Tyr Ser Ser Ala Met	
540	545
550	
ctg gaa agt tta tta cca ggc att cgt gac ctt tct ctg ccc cct gtg	1792
Leu Glu Ser Leu Leu Pro Gly Ile Arg Asp Leu Ser Leu Pro Pro Val	
555	560
565	
gat cga ctt gga tta cag aat gac ctc ttc tcc ttg gct cga gct gga	1840
Asp Arg Leu Gly Leu Gln Asn Asp Leu Phe Ser Leu Ala Arg Ala Gly	
570	575
580	585
atc att agc act gta gag gtt cta aaa gtc atg gag gct ttt gtg aat	1888
Ile Ile Ser Thr Val Glu Val Leu Lys Val Met Glu Ala Phe Val Asn	
590	595
600	
gag ccc aat tat act gta tgg agc gac ctg agc tgt aac ctg ggg att	1936

Glu Pro Asn Tyr Thr Val Trp Ser Asp Leu Ser Cys Asn Leu Gly Ile	
605	610
615	
ctc tca act ctc ttg tcc cac aca gac ttc tat gag gaa atc cag gag	1984
Leu Ser Thr Leu Leu Ser His Thr Asp Phe Tyr Glu Glu Ile Gln Glu	
620	625
630	
ttt gtg aaa gat gtc ttt tca cct ata ggg gag aga ctg ggc tgg gac	2032
Phe Val Lys Asp Val Phe Ser Pro Ile Gly Glu Arg Leu Gly Trp Asp	
635	640
645	
ccc aaa cct gga gaa ggt cat ctc gat gca ctc ctg agg ggc ttg gtt	2080
Pro Lys Pro Gly Glu Gly His Leu Asp Ala Leu Leu Arg Gly Leu Val	
650	655
660	665
ctg gga aaa cta gga aaa gca gga cat aag gca acg tta gaa gaa gcc	2128
Leu Gly Lys Leu Gly Lys Ala Gly His Lys Ala Thr Leu Glu Glu Ala	
670	675
680	
cgt cgt cgg ttt aag gac cac gtg gaa gga aaa cag att ctc tcc gct	2176
Arg Arg Arg Phe Lys Asp His Val Glu Gly Lys Gln Ile Leu Ser Ala	
685	690
695	
gat ctg agg agt cct gtc tat ctg act gtt ttg aag cat ggt gat ggc	2224
Asp Leu Arg Ser Pro Val Tyr Leu Thr Val Leu Lys His Gly Asp Gly	
700	705
710	
act act tta gat att atg tta aaa ctt cat aaa caa gca gat atg caa	2272
Thr Thr Leu Asp Ile Met Leu Lys Leu His Lys Gln Ala Asp Met Gln	
715	720
725	
gaa gag aaa aac cga atc gaa aga gtc ctt ggc gct act ctt ttg cct	2320
Glu Glu Lys Asn Arg Ile Glu Arg Val Leu Gly Ala Thr Leu Leu Pro	
730	735
740	745

gac ctg att caa aaa gtc ctc acg ttt gca ctt tca gaa gag gta cgt	2368
Asp Leu Ile Gln Lys Val Leu Thr Phe Ala Leu Ser Glu Glu Val Arg	
750 755 760	
cca cag gac act gta tcg gta att ggt gga gta gct gga ggc agc aag	2416
Pro Gln Asp Thr Val Ser Val Ile Gly Gly Val Ala Gly Gly Ser Lys	
765 770 775	
cat ggt agg aaa gct gct tgg aaa ttc ata aag gac aac tgg gaa gaa	2464
His Gly Arg Lys Ala Ala Trp Lys Phe Ile Lys Asp Asn Trp Glu Glu	
780 785 790	
ctt tat aac cga tac cag gga gga ttc tta ata tcc aga cta ata aag	2512
Leu Tyr Asn Arg Tyr Gln Gly Gly Phe Leu Ile Ser Arg Leu Ile Lys	
795 800 805	
cta tca gtt gag gga ttt gca gtt gat aaa atg gct gga gag gtt aag	2560
Leu Ser Val Glu Gly Phe Ala Val Asp Lys Met Ala Gly Glu Val Lys	
810 815 820 825	
gct ttc ttc gag agt cac cca gct cct tca gct gag cgt acc atc cag	2608
Ala Phe Phe Glu Ser His Pro Ala Pro Ser Ala Glu Arg Thr Ile Gln	
830 835 840	
cag tgt tgt gaa aat att ctg ctg aat gct gcc tgg cta aag cga gat	2656
Gln Cys Cys Glu Asn Ile Leu Leu Asn Ala Ala Trp Leu Lys Arg Asp	
845 850 855	
gct gag agc atc cac cag tac ctc ctt cag cgg aag gcc tca cca ccc	2704
Ala Glu Ser Ile His Gln Tyr Leu Leu Gln Arg Lys Ala Ser Pro Pro	
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aca gtg tgaatcctga ggtgccgcca ttggcggttc tgctgcttcg ctgcaggat	2760
Thr Val	
875	



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<210> 10

<211> 875

<212> PRT

<213> Homo sapiens

<400> 10

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1 5 10 15

Ile Asn Tyr Ser Leu Cys Leu Lys Pro Asp Leu Leu Asp Phe Thr Phe

20 25 30

Glu Gly Lys Leu Glu Ala Ala Ala Gln Val Arg Gln Ala Thr Asn Gln

35 40 45

Ile Val Met Asn Cys Ala Asp Ile Asp Ile Ile Thr Ala Ser Tyr Ala

50 55 60

Pro Glu Gly Asp Glu Glu Ile His Ala Thr Gly Phe Asn Tyr Gln Asn

65 70 75 80

Glu Asp Glu Lys Val Thr Leu Ser Phe Pro Ser Thr Leu Gln Thr Gly

85 90 95

Thr Gly Thr Leu Lys Ile Asp Phe Val Gly Glu Leu Asn Asp Lys Met

100 105 110

Lys Gly Phe Tyr Arg Ser Lys Tyr Thr Thr Pro Ser Gly Glu Val Arg

115 120 125

Tyr Ala Ala Val Thr Gln Phe Glu Ala Thr Asp Ala Arg Arg Ala Phe

130 135 140

Pro Cys Trp Asp Glu Pro Ala Ile Lys Ala Thr Phe Asp Ile Ser Leu

145 150 155 160

Val Val Pro Lys Asp Arg Val Ala Leu Ser Asn Met Asn Val Ile Asp

165 170 175

Arg Lys Pro Tyr Pro Asp Asp Glu Asn Leu Val Glu Val Lys Phe Ala

180 185 190

Arg Thr Pro Val Met Ser Thr Tyr Leu Val Ala Phe Val Val Gly Glu

195	200	205
Tyr Asp Phe Val Glu Thr Arg Ser Lys Asp Gly Val Cys Val Arg Val		
210	215	220
Tyr Thr Pro Val Gly Lys Ala Glu Gln Gly Lys Phe Ala Leu Glu Val		
225	230	235
Ala Ala Lys Thr Leu Pro Phe Tyr Lys Asp Tyr Phe Asn Val Pro Tyr		
245	250	255
Pro Leu Pro Lys Ile Asp Leu Ile Ala Ile Ala Asp Phe Ala Ala Gly		
260	265	270
Ala Met Glu Asn Trp Gly Leu Val Thr Tyr Arg Glu Thr Ala Leu Leu		
275	280	285
Ile Asp Pro Lys Asn Ser Cys Ser Ser Ser Arg Gln Trp Val Ala Leu		
290	295	300
Val Val Gly His Glu Leu Ala His Gln Trp Phe Gly Asn Leu Val Thr		
305	310	315
Met Glu Trp Trp Thr His Leu Trp Leu Asn Glu Gly Phe Ala Ser Trp		
325	330	335
Ile Glu Tyr Leu Cys Val Asp His Cys Phe Pro Glu Tyr Asp Ile Trp		
340	345	350
Thr Gln Phe Val Ser Ala Asp Tyr Thr Arg Ala Gln Glu Leu Asp Ala		
355	360	365
Leu Asp Asn Ser His Pro Ile Glu Val Ser Val Gly His Pro Ser Glu		
370	375	380
Val Asp Glu Ile Phe Asp Ala Ile Ser Tyr Ser Lys Gly Ala Ser Val		
385	390	395
Ile Arg Met Leu His Asp Tyr Ile Gly Asp Lys Asp Phe Lys Lys Gly		
405	410	415

Met Asn Met Tyr Leu Thr Lys Phe Gln Gln Lys Asn Ala Ala Thr Glu  
420 425 430  
Asp Leu Trp Glu Ser Leu Glu Asn Ala Ser Gly Lys Pro Ile Ala Ala  
435 440 445  
Val Met Asn Thr Trp Thr Lys Gln Met Gly Phe Pro Leu Ile Tyr Val  
450 455 460  
Glu Ala Glu Gln Val Glu Asp Asp Arg Leu Leu Arg Leu Ser Gln Lys  
465 470 475 480  
Lys Phe Cys Ala Gly Gly Ser Tyr Val Gly Glu Asp Cys Pro Gln Trp  
485 490 495  
Met Val Pro Ile Thr Ile Ser Thr Ser Glu Asp Pro Asn Gln Ala Lys  
500 505 510  
Leu Lys Ile Leu Met Asp Lys Pro Glu Met Asn Val Val Leu Lys Asn  
515 520 525  
Val Lys Pro Asp Gln Trp Val Lys Leu Asn Leu Gly Thr Val Gly Phe  
530 535 540  
Tyr Arg Thr Gln Tyr Ser Ser Ala Met Leu Glu Ser Leu Leu Pro Gly  
545 550 555 560  
Ile Arg Asp Leu Ser Leu Pro Pro Val Asp Arg Leu Gly Leu Gln Asn  
565 570 575  
Asp Leu Phe Ser Leu Ala Arg Ala Gly Ile Ile Ser Thr Val Glu Val  
580 585 590  
Leu Lys Val Met Glu Ala Phe Val Asn Glu Pro Asn Tyr Thr Val Trp  
595 600 605  
Ser Asp Leu Ser Cys Asn Leu Gly Ile Leu Ser Thr Leu Leu Ser His  
610 615 620

Thr	Asp	Phe	Tyr	Glu	Glu	Ile	Gln	Glu	Phe	Val	Lys	Asp	Val	Phe	Ser
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Pro	Ile	Gly	Glu	Arg	Leu	Gly	Trp	Asp	Pro	Lys	Pro	Gly	Glu	Gly	His
				645					650					655	
Leu	Asp	Ala	Leu	Leu	Arg	Gly	Leu	Val	Leu	Gly	Lys	Leu	Gly	Lys	Ala
		660						665						670	
Gly	His	Lys	Ala	Thr	Leu	Glu	Glu	Ala	Arg	Arg	Arg	Phe	Lys	Asp	His
		675						680						685	
Val	Glu	Gly	Lys	Gln	Ile	Leu	Ser	Ala	Asp	Leu	Arg	Ser	Pro	Val	Tyr
		690						695						700	
Leu	Thr	Val	Leu	Lys	His	Gly	Asp	Gly	Thr	Thr	Leu	Asp	Ile	Met	Leu
705					710									715	720
Lys	Leu	His	Lys	Gln	Ala	Asp	Met	Gln	Glu	Glu	Lys	Asn	Arg	Ile	Glu
				725						730				735	
Arg	Val	Leu	Gly	Ala	Thr	Leu	Leu	Pro	Asp	Leu	Ile	Gln	Lys	Val	Leu
			740							745				750	
Thr	Phe	Ala	Leu	Ser	Glu	Glu	Val	Arg	Pro	Gln	Asp	Thr	Val	Ser	Val
			755							760				765	
Ile	Gly	Gly	Val	Ala	Gly	Gly	Ser	Lys	His	Gly	Arg	Lys	Ala	Ala	Trp
		770								775				780	
Lys	Phe	Ile	Lys	Asp	Asn	Trp	Glu	Glu	Leu	Tyr	Asn	Arg	Tyr	Gln	Gly
785					790									795	800
Gly	Phe	Leu	Ile	Ser	Arg	Leu	Ile	Lys	Leu	Ser	Val	Glu	Gly	Phe	Ala
				805										810	815
Val	Asp	Lys	Met	Ala	Gly	Glu	Val	Lys	Ala	Phe	Phe	Glu	Ser	His	Pro
				820										825	830
Ala	Pro	Ser	Ala	Glu	Arg	Thr	Ile	Gln	Gln	Cys	Cys	Glu	Asn	Ile	Leu

835 840 845  
 Leu Asn Ala Ala Trp Leu Lys Arg Asp Ala Glu Ser Ile His Gln Tyr

850 855 860  
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865 870 875

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<211> 2007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1124).. (1330)

<400> 11

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 acacctacga tgtgccaggc acttgtttag gcgcttttat atagatccic gttaggatga 1080  
 gactaaggga tgaggacatc tctttataaa aggcccctaa gla atg gat aaa cag 1135

Met Asp Lys Gln

1

aaa cac tta gag gtg aga agg tct gtc ttc aag atc caa ggt aag att 1183  
 Lys His Leu Glu Val Arg Arg Ser Val Phe Lys Ile Gln Gly Lys Ile  
 5 10 15 20

gcc ttc agt ctg atg ttt gtt ctc aag gac tta tcc cct aca ata ttc 1231  
 Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser Pro Thr Ile Phe  
 25 30 35

tcc cac tcc ata ctt ctc ctt cta ccc cac cat gtg ctc ccg tgc act 1279  
 Ser His Ser Ile Leu Leu Leu Leu Pro His His Val Leu Pro Cys Thr  
 40 45 50

cct cag atg gtc aga ggg gta acc caa gtc ctt aga gaa ttt ggg gac 1327  
 Pro Gln Met Val Arg Gly Val Thr Gln Val Leu Arg Glu Phe Gly Asp  
 55 60 65

caa tagaatagt gatgtgtgaa ttttctttaa aaaacttaag gagtctttgc 1380  
 Gln

tacctctgc tigttagatt gttttggcat tcalattaaa agccagcatc tcactattta 1440  
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<211> 69

<212> PRT

<213> Homo sapiens

<400> 12

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Gln Gly Lys Ile Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser

20 25 30

Pro Thr Ile Phe Ser His Ser Ile Leu Leu Leu Leu Pro His His Val

35 40 45

Leu Pro Cys Thr Pro Gln Met Val Arg Gly Val Thr Gln Val Leu Arg

50 55 60

Glu Phe Gly Asp Gln

65

<210> 13

<211> 1953

<212> DNA

<213> Homo sapiens



<220>

<221> CDS

<222> (135).. (1850)

<400> 13

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tcigtcccttc gacccgagcc ccgcgccctt tccgggaccc ctgccccgcg ggcagcgctg 120

ccaacctgcc ggcc atg gag acc ccg tcc cag cgg cgc gcc acc cgc agc 170

Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser

1 5 10

ggg gcg cag gcc agc tcc act ccg ctg tgc ccc acc cgc atc acc cgg 218

Gly Ala Gln Ala Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg

15 20 25

ctg cag gag aag gag gac ctg cag gag ctc aat gat cgc ttg gcg gtc 266

Leu Gln Glu Lys Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val

30 35 40

tac atc gac cgt gtg cgc tgc ctg gaa acg gag aac gca ggg ctg cgc 314

Tyr Ile Asp Arg Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg

45 50 55 60

ctt cgc atc acc gag tct gaa gag gtg gtc agc cgc gag gtg tcc ggc 362

Leu Arg Ile Thr Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly

65 70 75

atc aag gcc gcc tac gag gcc gag ctc ggg gat gcc cgc aag acc ctt 410

Ile Lys Ala Ala Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu

80 85 90

gac tca gta gcc aag gag cgc gcc cgc ctg cag ctg gag ctg agc aaa 458

Asp Ser Val Ala Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys

95	100	105	
gtg cgt gag gag ttt aag gag ctg aaa gcg cgc aat acc aag aag gag	506		
Val Arg Glu Glu Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu			
110	115	120	
ggt gac ctg ata gct gct cag gct cgg ctg aag gac ctg gag gct ctg	554		
Gly Asp Leu Ile Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu			
125	130	135	140
ctg aac tcc aag gag gcc gca ctg agc act gct ctc agt gag aag cgc	602		
Leu Asn Ser Lys Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg			
145	150	155	
acg ctg gag ggc gag ctg cat gat ctg cgg ggc cag gtg gcc aag ctt	650		
Thr Leu Glu Gly Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu			
160	165	170	
gag gca gcc cta ggt gag gcc aag aag caa ctt cag gat gag atg ctg	698		
Glu Ala Ala Leu Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu			
175	180	185	
cgg cgg gtg gat gct gag aac agg ctg cag acc atg aag gag gaa ctg	746		
Arg Arg Val Asp Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu			
190	195	200	
gac ttc cag aag aac atc tac agt gag gag ctg cgt gag acc aag cgc	794		
Asp Phe Gln Lys Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg			
205	210	215	220
cgt cat gag acc cga ctg gtg gag att gac aat ggg aag cag cgt gag	842		
Arg His Glu Thr Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu			
225	230	235	
ttt gag agc cgg ctg gcg gat gcg ctg cag gaa ctg cgg gcc cag cat	890		
Phe Glu Ser Arg Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His			

240	245	250	
gag gac cag gtg gag cag tat aag aag gag ctg gag aag act tat tct			938
Glu Asp Gln Val Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser			
255	260	265	
gcc aag ctg gac aat gcc agg cag tct gct gag agg aac agc aac ctg			986
Ala Lys Leu Asp Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu			
270	275	280	
gtg ggg gct gcc cac gag gag ctg cag cag tcg cgc atc cgc atc gac			1034
Val Gly Ala Ala His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp			
285	290	295	300
agc ctc tct gcc cag ctc agc cag ctc cag aag cag ctg gca gcc aag			1082
Ser Leu Ser Ala Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys			
305	310	315	
gag gcg aag ctt cga gac ctg gag gac tca ctg gcc cgt gag cgg gac			1130
Glu Ala Lys Leu Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp			
320	325	330	
acc agc cgg cgg ctg ctg gcg gaa aag gag cgg gag atg gcc gag atg			1178
Thr Ser Arg Arg Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met			
335	340	345	
cgg gca agg atg cag cag cag ctg gac gag tac cag gag ctt ctg gac			1226
Arg Ala Arg Met Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp			
350	355	360	
atc aag ctg gcc ctg gac atg gag atc cac gcc tac cgc aag ctc ttg			1274
Ile Lys Leu Ala Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu			
365	370	375	380
gag ggc gag gag gag agg cta cgc ctg tcc ccc agc cct acc tcg cag			1322

Glu Gly Glu Glu Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln	
385	390
395	
cgc agc cgt ggc cgt gct tcc tct cac tca tcc cag aca cag ggt ggg	1370
Arg Ser Arg Gly Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly	
400	405
410	
ggc agc gtc acc aaa aag cgc aaa ctg gag tcc act gag agc cgc agc	1418
Gly Ser Val Thr Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser	
415	420
425	
agc ttc tca cag cac gca cgc act agc ggg cgc gtg gcc gtg gag gag	1466
Ser Phe Ser Gln His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu	
430	435
440	
gtg gat gag gag ggc aag ttt gtc cgg ctg cgc aac aag tcc aat gag	1514
Val Asp Glu Glu Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu	
445	450
455	460
gac cag tcc atg ggc aat tgg cag atc aag cgc cag aat gga gat gat	1562
Asp Gln Ser Met Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp	
465	470
475	
ccc ttg ctg act tac cgg ttc cca cca aag ttc acc ctg aag gct ggg	1610
Pro Leu Leu Thr Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly	
480	485
490	
cag gtg gtg acg atc tgg gct gca gga gct ggg gcc acc cac agc ccc	1658
Gln Val Val Thr Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro	
495	500
505	
cct acc gac ctg gtg tgg aag gca cag aac acc tgg ggc tgc ggg aac	1706
Pro Thr Asp Leu Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn	
510	515
520	
agc ctg cgt acg gct ctc atc aac tcc act ggg gaa gaa gtg gcc atg	1754

Ser Leu Arg Thr Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met  
 525                      530                      535                      540  
 cgc aag ctg gtg cgc tca gtg act gtg gtt gag gac gac gag gat gag 1802  
 Arg Lys Leu Val Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu  
                          545                      550                      555  
 gat gga gat gac ctg ctc cat cac cac cac gtg agt ggt agc cgc cgc 1850  
 Asp Gly Asp Asp Leu Leu His His His His Val Ser Gly Ser Arg Arg  
                          560                      565                      570  
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<210> 14

<211> 572

<212> PRT

<213> Homo sapiens

<400> 14

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 Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys  
                          20                      25                      30  
 Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg  
                          35                      40                      45  
 Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr  
                          50                      55                      60  
 Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala  
                          65                      70                      75                      80  
 Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala

	85	90	95
Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu			
	100	105	110
Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile			
	115	120	125
Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys			
	130	135	140
Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly			
145	150	155	160
Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu			
	165	170	175
Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp			
	180	185	190
Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys			
	195	200	205
Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr			
	210	215	220
Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg			
225	230	235	240
Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val			
	245	250	255
Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp			
	260	265	270
Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala			
	275	280	285
His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala			

290	295	300	
Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu			
305	310	315	320
Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg			
	325	330	335
Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met			
	340	345	350
Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala			
	355	360	365
Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu			
	370	375	380
Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly			
385	390	395	400
Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr			
	405	410	415
Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln			
	420	425	430
His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu			
	435	440	445
Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met			
	450	455	460
Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr			
465	470	475	480
Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr			
	485	490	495
Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu			
	500	505	510

Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr

515

520

525

Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val

530

535

540

Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp

545

550

555

560

Leu Leu His His His His Val Ser Gly Ser Arg Arg

565

570

<210> 15

<211> 2865

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (240).. (1475)

<400> 15

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cgcccccaac tgaagctgca tcitcaaagcc gaagattcca gcagcccagg ggatttcaaa 120

gagctcagac tcagaggaac atctgcggag agacccccga agccctctcc agggcagttc 180

tcatccagac gctccgttag tgcagacagg agcgcgcagt ggccccggct cgccgcgcc 239

atg gag cgg atc ccc agc gcg caa cca ccc ccc gcc tgc ctg ccc aaa 287

Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys

1

5

10

15

gca ccg gga ctg gag cac cga gac cta cca ggg atg tac cct gcc cac 335

Ala Pro Gly Leu Glu His Arg Asp Leu Pro Gly Met Tyr Pro Ala His

20

25

30



atg tac caa gtg tac aag tca aga cgg gga ata aag cgg agc gag gac	383
Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp	
35 40 45	
agc aag gag acc tac aaa ttg ccg cac cgg ctg ttc gag aaa aag aga	431
Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg	
50 55 60	
cgt gac cgg att aac gag tgc atc gcc cag ctg aag gat ctg cta ccc	479
Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro	
65 70 75 80	
gaa cat ctg aaa ctt aca act ttg ggt cac ttg gaa aaa gca gtg gtt	527
Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val	
85 90 95	
ctt gaa ctt acc ttg aag cat gtg aaa gca cta aca aac cta att gat	575
Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp	
100 105 110	
cag cag cag cag aaa atc att gcc ctg cag agt ggt tta caa gct ggt	623
Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly	
115 120 125	
gag ctg tca ggg aga aat gtc gaa aca ggt caa gag atg ttc tgc tca	671
Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser	
130 135 140	
ggt ttc cag aca tgt gcc cgg gag gtg ctt cag tat ctg gcc aag cac	719
Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His	
145 150 155 160	
gag aac act cgg gac ctg aag tct tcg cag ctt gtc acc cac ctg cac	767
Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His	

165	170	175	
cgg gtg gtc tcg gag ctg ctg cag ggt ggt acc tcc agg aag cca tca	815		
Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser			
180	185	190	
gac cca gct ccc aaa gtg atg gac ttc aag gaa aaa ccc agc tct ccg	863		
Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro			
195	200	205	
gcc aaa ggt tcg gaa ggt cct ggg aaa aac tgc gtg cca gtc atc cag	911		
Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln			
210	215	220	
cgg act ttc gct cac tcg agt ggg gag cag agc ggc agc gac acg gac	959		
Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp			
225	230	235	240
aca gac agt ggc tat gga gga gat tcg gag aag ggc gac ttg cgc agt	1007		
Thr Asp Ser Gly Tyr Gly Gly Asp Ser Glu Lys Gly Asp Leu Arg Ser			
245	250	255	
gag cag ccg tgc ttc aaa agt gac cac gga cgc agg ttc acg atg gga	1055		
Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly			
260	265	270	
gaa agg atc ggc gca att aag caa gag tcc gaa gaa ccc ccc aca aaa	1103		
Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys			
275	280	285	
aag aac cgg atg cag ctt tcg gat gat gaa ggc cat ttc act agc agt	1151		
Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser			
290	295	300	
gac ctg atc agc tcc ccg ttc ctg ggc cca cac cca cac cag cct cct	1199		
Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro			

305	310	315	320	
ttc tgc ctg ccc ttc tac ctg atc cca cct tca gcg act gcc tac ctg	1247			
Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu				
325	330	335		
ccc atg ctg gag aag tgc tgg tat ccc acc tca gtg cca gtg cta tac	1295			
Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr				
340	345	350		
cca ggc ctc aac gcc tct gcc gca gcc ctc tct agc ttc atg aac cca	1343			
Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro				
355	360	365		
gac aag atc tcg gct ccc ttg ctc atg ccc cag aga ctc cct tct ccc	1391			
Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro				
370	375	380		
ttg cca gct cat ccg tcc gtc gac tct tct gtc ttg ctc caa gct ctg	1439			
Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu				
385	390	395	400	
aag cca atc ccc cct tta aac tta gaa acc aaa gac taaactctct	1485			
Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp				
405	410			
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caganncagg gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtatgtgcgt gtgcgtgcac	1665			
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tcaaaaagagg gctttccagg gctcagctcc caaccagctg ttaggacccc acccttttgc 1965  
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 ctgctaacat ggggagggta gcagacactg gcatagcacg gtagtgggtt gggggagggt 2085  
 ttccgcaggt ctgctcccca cccctgcctc ggaagaataa agagaatgta gtccctact 2145  
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<210> 16

<211> 412

<212> PRT

<213> Homo sapiens

<400> 16

Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys

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Ala Pro Gly Leu Glu His Arg Asp Leu Pro Gly Met Tyr Pro Ala His

20

25

30

Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp

35	40	45	
Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg			
50	55	60	
Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro			
65	70	75	80
Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val			
85	90	95	
Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp			
100	105	110	
Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly			
115	120	125	
Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser			
130	135	140	
Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His			
145	150	155	160
Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His			
165	170	175	
Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser			
180	185	190	
Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro			
195	200	205	
Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln			
210	215	220	
Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp			
225	230	235	240
Thr Asp Ser Gly Tyr Gly Gly Asp Ser Glu Lys Gly Asp Leu Arg Ser			
245	250	255	

Glu	Gln	Pro	Cys	Phe	Lys	Ser	Asp	His	Gly	Arg	Arg	Phe	Thr	Met	Gly
		260						265					270		
Glu	Arg	Ile	Gly	Ala	Ile	Lys	Gln	Glu	Ser	Glu	Glu	Pro	Pro	Thr	Lys
		275				280						285			
Lys	Asn	Arg	Met	Gln	Leu	Ser	Asp	Asp	Glu	Gly	His	Phe	Thr	Ser	Ser
	290					295					300				
Asp	Leu	Ile	Ser	Ser	Pro	Phe	Leu	Gly	Pro	His	Pro	His	Gln	Pro	Pro
305					310					315				320	
Phe	Cys	Leu	Pro	Phe	Tyr	Leu	Ile	Pro	Pro	Ser	Ala	Thr	Ala	Tyr	Leu
			325					330					335		
Pro	Met	Leu	Glu	Lys	Cys	Trp	Tyr	Pro	Thr	Ser	Val	Pro	Val	Leu	Tyr
		340						345					350		
Pro	Gly	Leu	Asn	Ala	Ser	Ala	Ala	Ala	Leu	Ser	Ser	Phe	Met	Asn	Pro
		355					360						365		
Asp	Lys	Ile	Ser	Ala	Pro	Leu	Leu	Met	Pro	Gln	Arg	Leu	Pro	Ser	Pro
	370					375					380				
Leu	Pro	Ala	His	Pro	Ser	Val	Asp	Ser	Ser	Val	Leu	Leu	Gln	Ala	Leu
385					390					395				400	
Lys	Pro	Ile	Pro	Pro	Leu	Asn	Leu	Glu	Thr	Lys	Asp				
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<210> 17

<211> 3817

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (164).. (2665)

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tcttaactag tgtaggaaaa cggctcaacc caccgctgcc gaa atg aag tat aag 175

Met Lys Tyr Lys

1

aat ctt atg gca agg gcc tta tat gac aat gtc cca gag tgt gcc gag 223  
Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro Glu Cys Ala Glu

5 10 15 20

gaa ctg gcc ttt cgc aag gga gac atc ctg acc gtc ata gag cag aac 271  
Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val Ile Glu Gln Asn

25 30 35

aca ggg gga ctg gaa gga tgg tgg ctg tgc tgc tta cac ggt cgg caa 319  
Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu His Gly Arg Gln

40 45 50

ggc att gtc cca ggc aac cgg gtg aag ctt ctg att ggt ccc atg cag 367  
Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile Gly Pro Met Gln

55 60 65

gag act gcc tcc agt cac gag cag cct gcc tct gga ctg atg cag cag 415  
Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly Leu Met Gln Gln

70 75 80

acc ttt ggc caa cag aag ctc tat caa gtg cca aac cca cag gct gct 463  
Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn Pro Gln Ala Ala

85 90 95 100

ccc cga gac acc atc tac caa gtg cca cct tcc tac caa aat cag gga 511

Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr Gln Asn Gln Gly	
105	110
115	
att tac caa gtc ccc act ggc cac ggc acc caa gaa caa gag gta tat	559
Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu Gln Glu Val Tyr	
120	125
130	
cag gtg cca cca tca gtg cag aga agc att ggg gga acc agt ggg ccc	607
Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly Thr Ser Gly Pro	
135	140
145	
cac gtg ggt aaa aag gtg ata acc ccc gtg agg aca ggc cat ggc tac	655
His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr Gly His Gly Tyr	
150	155
160	
gta tac gag tac cca tcc aga tac caa aag gat gtc tat gat atc cct	703
Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val Tyr Asp Ile Pro	
165	170
175	180
cct tct cat acc act caa ggg gta tac gac atc cct ccc tca tca gca	751
Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro Pro Ser Ser Ala	
185	190
195	
aaa ggc cct gtg ttt tca gtt cca gtg gga gag ata aaa cct caa ggg	799
Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile Lys Pro Gln Gly	
200	205
210	
gtg tat gac atc ccg cct aca aaa ggg gta tat gcc att ccg ccc tct	847
Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala Ile Pro Pro Ser	
215	220
225	
gct tgc cgg gat gaa gca ggg ctt agg gaa aaa gac tat gac ttc ccc	895
Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp Tyr Asp Phe Pro	
230	235
240	
cct ccc atg aga caa gct gga agg ccg gac ctc aga ccg gag ggg gtt	943



Pro	Pro	Met	Arg	Gln	Ala	Gly	Arg	Pro	Asp	Leu	Arg	Pro	Glu	Gly	Val	
245					250					255					260	
tat	gac	att	cct	cca	acc	tgc	acc	aag	cca	gca	ggg	aag	gac	ctt	cat	991
Tyr	Asp	Ile	Pro	Pro	Thr	Cys	Thr	Lys	Pro	Ala	Gly	Lys	Asp	Leu	His	
				265					270					275		
gta	aaa	tac	aac	tgt	gac	att	cca	gga	gct	gca	gaa	ccg	gtg	gct	cga	1039
Val	Lys	Tyr	Asn	Cys	Asp	Ile	Pro	Gly	Ala	Ala	Glu	Pro	Val	Ala	Arg	
				280					285					290		
agg	cac	cag	agc	ctg	tcc	ccg	aat	cac	cca	ccc	ccg	caa	ctc	gga	cag	1087
Arg	His	Gln	Ser	Leu	Ser	Pro	Asn	His	Pro	Pro	Pro	Gln	Leu	Gly	Gln	
				295					300					305		
tca	gtg	ggc	tct	cag	aac	gac	gca	tat	gat	gtc	ccc	cga	ggc	gtt	cag	1135
Ser	Val	Gly	Ser	Gln	Asn	Asp	Ala	Tyr	Asp	Val	Pro	Arg	Gly	Val	Gln	
				310					315					320		
ttt	ctt	gag	cca	cca	gca	gaa	acc	agt	gag	aaa	gca	aac	ccc	cag	gaa	1183
Phe	Leu	Glu	Pro	Pro	Ala	Glu	Thr	Ser	Glu	Lys	Ala	Asn	Pro	Gln	Glu	
325					330					335				340		
agg	gat	ggt	gtt	tat	gat	gtc	cct	ctg	cat	aac	ccg	cca	gat	gct	aaa	1231
Arg	Asp	Gly	Val	Tyr	Asp	Val	Pro	Leu	His	Asn	Pro	Pro	Asp	Ala	Lys	
				345					350					355		
ggc	tct	cgg	gac	tig	gtg	gat	ggg	atc	aac	cga	tig	tct	ttc	tcc	agt	1279
Gly	Ser	Arg	Asp	Leu	Val	Asp	Gly	Ile	Asn	Arg	Leu	Ser	Phe	Ser	Ser	
				360					365					370		
aca	ggc	agc	acc	cgg	agt	aac	atg	tcc	acg	tct	tcc	acc	tcc	tcc	aag	1327
Thr	Gly	Ser	Thr	Arg	Ser	Asn	Met	Ser	Thr	Ser	Ser	Thr	Ser	Ser	Lys	
				375					380					385		

gag tcc tca ctg tca gcc tcc cca gct cag gac aaa agg ctc ttc ctg	1375
Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys Arg Leu Phe Leu	
390 395 400	
gat cca gac aca gct att gag aga ctt cag cgg ctc cag cag gcc ctt	1423
Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu Gln Gln Ala Leu	
405 410 415 420	
gag atg ggt gtc tcc agc cta atg gca ctg gtc act acc gac tgg cgg	1471
Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr Thr Asp Trp Arg	
425 430 435	
tgt tac gga tat atg gaa aga cac atc aat gaa ata cgc aca gca gtg	1519
Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile Arg Thr Ala Val	
440 445 450	
gac aag gtg gag ctg ttc ctg aag gag tac ctc cac ttt gtc aag gga	1567
Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His Phe Val Lys Gly	
455 460 465	
gct gtt gca aat gct gcc tgc ctc ccg gaa ctc atc ctc cac aac aag	1615
Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile Leu His Asn Lys	
470 475 480	
atg aag cgg gag ctg caa cga gtc gaa gac tcc cac cag atc ctg agt	1663
Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His Gln Ile Leu Ser	
485 490 495 500	
caa acc agc cat gac tta aat gag tgc agc tgg tcc ctg aat atc ttg	1711
Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser Leu Asn Ile Leu	
505 510 515	
gcc atc aac aag ccc cag aac aag tgt gac gat ctg gac cgg ttt gtg	1759
Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu Asp Arg Phe Val	
520 525 530	

atg gtg gca aag acg gtg ccc gat gac gcc aag cag ctc acc aca acc	1807
Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln Leu Thr Thr Thr	
535 540 545	
atc aac acc aac gca gag gcc ctc ttc aga ccc ggc cct ggc agc ttg	1855
Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly Pro Gly Ser Leu	
550 555 560	
cat ctg aag aat ggg ccg gag agc atc atg aac tca acg gag tac cca	1903
His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser Thr Glu Tyr Pro	
565 570 575 580	
cac ggt ggc tcc cag gga cag ctg ctg cat cct ggt gac cac aag gcc	1951
His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly Asp His Lys Ala	
585 590 595	
cag gcc cac aac aag gca ctg ccc cca ggc ctg agc aag gag cag gcc	1999
Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser Lys Glu Gln Ala	
600 605 610	
cct gac tgt agc agc agt gat ggt tct gag agg agc tgg atg gat gac	2047
Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser Trp Met Asp Asp	
615 620 625	
tac gat tac gtc cac cta cag ggt aag gag gag ttt gag agg caa cag	2095
Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe Glu Arg Gln Gln	
630 635 640	
aaa gag cta ttg gaa aaa gag aat atc atg aaa cag aac aag atg cag	2143
Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln Asn Lys Met Gln	
645 650 655 660	
ctg gaa cat cat cag ctg agc cag ttc cag ctg ttg gaa caa gag att	2191
Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu Glu Gln Glu Ile	

665	670	675	
aca aag ccc gtg gag aat gac atc tcg aag tgg aag ccc tct cag agc	2239		
Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys Pro Ser Gln Ser			
680	685	690	
cta ccc acc aca aac agt ggc gtg agt gct cag gat cgg cag ttg ctg	2287		
Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp Arg Gln Leu Leu			
695	700	705	
tgc ttc tac tat gac caa tgt gag acc cat ttc att tcc ctt ctc aac	2335		
Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile Ser Leu Leu Asn			
710	715	720	
gcc att gac gca ctc ttc agt tgt gtc agc tca gcc cag ccc ccg cga	2383		
Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala Gln Pro Pro Arg			
725	730	735	740
atc ttc gtg gca cac agc aag ttt gtc atc ctc agt gca cac aaa ctg	2431		
Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser Ala His Lys Leu			
745	750	755	
gtg ttc att gga gac acg ctg aca cgg cag gtg act gcc cag gac att	2479		
Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr Ala Gln Asp Ile			
760	765	770	
cgc aac aaa gtc atg aac tcc agc aac cag ctc tgc gag cag ctc aag	2527		
Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys Glu Gln Leu Lys			
775	780	785	
act ata gtc atg gca acc aag atg gcc gcc ctc cat tac ccc agc acc	2575		
Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His Tyr Pro Ser Thr			
790	795	800	
acg gcc ctg cag gaa atg gtg cac caa gtg aca gac ctt tct aga aat	2623		
Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp Leu Ser Arg Asn			

805	810	815	820	
gcc cag ctg ttc aag cgc tct ttg ctg gag atg gca acg ttc				2665
Ala Gln Leu Phe Lys Arg Ser Leu Leu Glu Met Ala Thr Phe				
	825	830		
tgagaagaaa	aaaaagagga	aggggactgc	gttaacggtt	actaaggaaa actggaaata 2725
ctgtctgggt	tttgtaaagt	ttaactatgt	ttgtagataa	ttttatataa aaatgaaata 2785
ttttaacatt	ttatgggtca	gacaactttc	agaaattcag	ggagctggag agggaaatct 2845
ttttttcccc	cctgagtggt	cttatgtata	cacagaagta	tctgagacat aaactgtaca 2905
gaaaacttgt	ccacgtcctt	ttgtatgccc	atgtattcat	gtttttgttt gtagatgttt 2965
gtctgatgca	tttcattaaa	aaaaaaacca	tgaattacga	agcaccttag taagcacctt 3025
ctaattgctg	atTTTTTTTg	ttgttggtta	aaacatccag	ctggttataa tattgtttctc 3085
cacgtccttg	tgatgattct	gagcctggca	ctgggaatct	gggaagcata gtttatttgc 3145
aagtgttcac	cttccaaatc	atgaggcata	gcatgactta	ticttgtttt gaaaactctt 3205
ttcaaaactg	accatcttaa	acacatgatg	gccaagtgcc	acaaagccct ctgtcggaga 3265
catttacgaa	tatatagttg	gatccaagtc	tcgatagtta	ggcgttggag ggaagagaga 3325
ccagagagtt	tagaggccag	gaccacagtt	aggattgggt	tgtttcaata ctgagagaca 3385
gctacaataa	aaggagagca	attgccctcc	tggggctgtt	caatcttctg catttgtgag 3445
tggttcagtc	atgaggtttt	ccaaaagatg	tttttagagt	tgtaaaaacc atatitgcag 3505
caaagattta	caaaggcgta	tcagactatg	attgttcacc	aaaatagggg aatggtttga 3565
tccgccagtt	gcaagtagag	gcccttctga	ctcttaatat	tcactttggt gctactaccc 3625
ccattaccig	aggaactggc	caggccttgc	atcatggaac	tatagagcta ccagacatat 3685
cctgctctct	aagggaatgt	attgctatct	tgcaccttct	ttaaaactca aaaaacatat 3745
gcagacctga	cactcaagag	tggctagcta	cacagagctc	atctaatttt tgcaacttcc 3805
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<210> 18

<211> 834

<212> PRT

<213> Homo sapiens

<400> 18

Met	Lys	Tyr	Lys	Asn	Leu	Met	Ala	Arg	Ala	Leu	Tyr	Asp	Asn	Val	Pro
1				5					10					15	
Glu	Cys	Ala	Glu	Glu	Leu	Ala	Phe	Arg	Lys	Gly	Asp	Ile	Leu	Thr	Val
			20					25					30		
Ile	Glu	Gln	Asn	Thr	Gly	Gly	Leu	Glu	Gly	Trp	Trp	Leu	Cys	Ser	Leu
		35					40					45			
His	Gly	Arg	Gln	Gly	Ile	Val	Pro	Gly	Asn	Arg	Val	Lys	Leu	Leu	Ile
	50					55					60				
Gly	Pro	Met	Gln	Glu	Thr	Ala	Ser	Ser	His	Glu	Gln	Pro	Ala	Ser	Gly
65				70						75				80	
Leu	Met	Gln	Gln	Thr	Phe	Gly	Gln	Gln	Lys	Leu	Tyr	Gln	Val	Pro	Asn
			85						90					95	
Pro	Gln	Ala	Ala	Pro	Arg	Asp	Thr	Ile	Tyr	Gln	Val	Pro	Pro	Ser	Tyr
		100						105						110	
Gln	Asn	Gln	Gly	Ile	Tyr	Gln	Val	Pro	Thr	Gly	His	Gly	Thr	Gln	Glu
		115					120						125		
Gln	Glu	Val	Tyr	Gln	Val	Pro	Pro	Ser	Val	Gln	Arg	Ser	Ile	Gly	Gly
	130					135							140		
Thr	Ser	Gly	Pro	His	Val	Gly	Lys	Lys	Val	Ile	Thr	Pro	Val	Arg	Thr
145				150						155				160	
Gly	His	Gly	Tyr	Val	Tyr	Glu	Tyr	Pro	Ser	Arg	Tyr	Gln	Lys	Asp	Val
				165						170				175	
Tyr	Asp	Ile	Pro	Pro	Ser	His	Thr	Thr	Gln	Gly	Val	Tyr	Asp	Ile	Pro

180	185	190	
Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile			
195	200	205	
Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala			
210	215	220	
Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp			
225	230	235	240
Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg			
245	250	255	
Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly			
260	265	270	
Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu			
275	280	285	
Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro			
290	295	300	
Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro			
305	310	315	320
Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala			
325	330	335	
Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro			
340	345	350	
Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu			
355	360	365	
Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser			
370	375	380	
Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys			
385	390	395	400

Arg Leu Phe Leu Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu			
405	410	415	
Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr			
420	425	430	
Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile			
435	440	445	
Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His			
450	455	460	
Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile			
465	470	475	480
Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His			
485	490	495	
Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser			
500	505	510	
Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu			
515	520	525	
Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln			
530	535	540	
Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly			
545	550	555	560
Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser			
565	570	575	
Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly			
580	585	590	
Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser			
595	600	605	



Lys	Glu	Gln	Ala	Pro	Asp	Cys	Ser	Ser	Ser	Asp	Gly	Ser	Glu	Arg	Ser
610						615									620
Trp	Met	Asp	Asp	Tyr	Asp	Tyr	Val	His	Leu	Gln	Gly	Lys	Glu	Glu	Phe
625						630									640
Glu	Arg	Gln	Gln	Lys	Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Met	Lys	Gln
						645									655
Asn	Lys	Met	Gln	Leu	Glu	His	His	Gln	Leu	Ser	Gln	Phe	Gln	Leu	Leu
						660									670
Glu	Gln	Glu	Ile	Thr	Lys	Pro	Val	Glu	Asn	Asp	Ile	Ser	Lys	Trp	Lys
						675									685
Pro	Ser	Gln	Ser	Leu	Pro	Thr	Thr	Asn	Ser	Gly	Val	Ser	Ala	Gln	Asp
						690									700
Arg	Gln	Leu	Leu	Cys	Phe	Tyr	Tyr	Asp	Gln	Cys	Glu	Thr	His	Phe	Ile
705						710									720
Ser	Leu	Leu	Asn	Ala	Ile	Asp	Ala	Leu	Phe	Ser	Cys	Val	Ser	Ser	Ala
						725									735
Gln	Pro	Pro	Arg	Ile	Phe	Val	Ala	His	Ser	Lys	Phe	Val	Ile	Leu	Ser
						740									750
Ala	His	Lys	Leu	Val	Phe	Ile	Gly	Asp	Thr	Leu	Thr	Arg	Gln	Val	Thr
						755									765
Ala	Gln	Asp	Ile	Arg	Asn	Lys	Val	Met	Asn	Ser	Ser	Asn	Gln	Leu	Cys
						770									780
Glu	Gln	Leu	Lys	Thr	Ile	Val	Met	Ala	Thr	Lys	Met	Ala	Ala	Leu	His
785						790									800
Tyr	Pro	Ser	Thr	Thr	Ala	Leu	Gln	Glu	Met	Val	His	Gln	Val	Thr	Asp
						805									815
Leu	Ser	Arg	Asn	Ala	Gln	Leu	Phe	Lys	Arg	Ser	Leu	Leu	Glu	Met	Ala

820

825

830

Thr Phe

&lt;210&gt; 19

&lt;211&gt; 567

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (36).. (506)

&lt;400&gt; 19

tgtgacgcct gcagggctgg gacctgacgg tgaag atg ctg gcg ggc aac gaa 53

Met Leu Ala Gly Asn Glu

1

5

ttc cag gtg tcc ctg agc agc tcc atg tcg gtg tca gag ctg aag gcg 101

Phe Gln Val Ser Leu Ser Ser Ser Met Ser Val Ser Glu Leu Lys Ala

10

15

20

cag atc acc cag aac att ggc gtg cac gcc ttc cag cag cgt ctg gct 149

Gln Ile Thr Gln Asn Ile Gly Val His Ala Phe Gln Gln Arg Leu Ala

25

30

35

gtc cac ccg agc ggt gtg gcg ctg cag gac agg gtc ccc ctt gcc agc 197

Val His Pro Ser Gly Val Ala Leu Gln Asp Arg Val Pro Leu Ala Ser

40

45

50

cag ggc ctg ggc cct ggc agc acg gtc ctg ctg gtg gtg gac aaa tgc 245

Gln Gly Leu Gly Pro Gly Ser Thr Val Leu Leu Val Val Asp Lys Cys

55

60

65

70

gac gaa cct ctg agc atc ctg gtg agg aat aac aag ggc cgc agc agc 293

Asp	Glu	Pro	Leu	Ser	Ile	Leu	Val	Arg	Asn	Asn	Lys	Gly	Arg	Ser	Ser		
				75					80					85			
acc	tac	gag	gtg	cgg	ctg	acg	cag	acc	gtg	gcc	cac	ctg	aag	cag	caa	341	
Thr	Tyr	Glu	Val	Arg	Leu	Thr	Gln	Thr	Val	Ala	His	Leu	Lys	Gln	Gln		
				90					95					100			
gtg	agc	ggg	ctg	gag	ggg	gtg	cag	gac	gac	ctg	ttc	tgg	ctg	acc	ttc	389	
Val	Ser	Gly	Leu	Glu	Gly	Val	Gln	Asp	Asp	Leu	Phe	Trp	Leu	Thr	Phe		
				105					110					115			
gag	ggg	aag	ccc	ctg	gag	gac	cag	ctc	ccg	ctg	ggg	gag	tac	ggc	ctc	437	
Glu	Gly	Lys	Pro	Leu	Glu	Asp	Gln	Leu	Pro	Leu	Gly	Glu	Tyr	Gly	Leu		
				120					125					130			
aag	ccc	ctg	agc	acc	gtg	ttc	atg	aat	ctg	cgc	ctg	cgg	gga	ggc	ggc	485	
Lys	Pro	Leu	Ser	Thr	Val	Phe	Met	Asn	Leu	Arg	Leu	Arg	Gly	Gly	Gly		
				135					140					145			
aca	gag	cct	ggc	ggg	cgg	agc	taagggcctc	caccagcatc	cgagcaggat							536	
Thr	Glu	Pro	Gly	Gly	Arg	Ser											
				155													
caagggccgg	aataaaaggct	gttgtaagag	a													567	

Met Leu Ala Gly Asn Glu Phe Gln Val Ser Leu Ser Ser Ser Met Ser  
1 5 10 15  
Val Ser Glu Leu Lys Ala Gln Ile Thr Gln Asn Ile Gly Val His Ala

20	25	30
Phe Gln Gln Arg Leu Ala Val His Pro Ser Gly Val Ala Leu Gln Asp		
35	40	45
Arg Val Pro Leu Ala Ser Gln Gly Leu Gly Pro Gly Ser Thr Val Leu		
50	55	60
Leu Val Val Asp Lys Cys Asp Glu Pro Leu Ser Ile Leu Val Arg Asn		
65	70	75
Asn Lys Gly Arg Ser Ser Thr Tyr Glu Val Arg Leu Thr Gln Thr Val		
85	90	95
Ala His Leu Lys Gln Gln Val Ser Gly Leu Glu Gly Val Gln Asp Asp		
100	105	110
Leu Phe Trp Leu Thr Phe Glu Gly Lys Pro Leu Glu Asp Gln Leu Pro		
115	120	125
Leu Gly Glu Tyr Gly Leu Lys Pro Leu Ser Thr Val Phe Met Asn Leu		
130	135	140
Arg Leu Arg Gly Gly Gly Thr Glu Pro Gly Gly Arg Ser		
145	150	155

<210> 21

<211> 5095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14).. (2593)

<400> 21

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gcc	ttg	ctc	ctc	gcc	gcg	gcg	ggg	act	gca	gtg	ggc	gac	aga	tgt	gaa	97
Ala	Leu	Leu	Leu	Ala	Ala	Ala	Gly	Thr	Ala	Val	Gly	Asp	Arg	Cys	Glu	
15				20				25								
aga	aac	gag	ttc	cag	tgc	caa	gac	ggg	aaa	tgc	atc	tcc	tac	aag	tgg	145
Arg	Asn	Glu	Phe	Gln	Cys	Gln	Asp	Gly	Lys	Cys	Ile	Ser	Tyr	Lys	Trp	
30				35				40								
gtc	tgc	gat	ggc	agc	gct	gag	tgc	cag	gat	ggc	tct	gat	gag	tcc	cag	193
Val	Cys	Asp	Gly	Ser	Ala	Glu	Cys	Gln	Asp	Gly	Ser	Asp	Glu	Ser	Gln	
45				50				55				60				
gag	acg	tgc	ttg	tct	gtc	acc	tgc	aaa	tcc	ggg	gac	ttc	agc	tgt	ggg	241
Glu	Thr	Cys	Leu	Ser	Val	Thr	Cys	Lys	Ser	Gly	Asp	Phe	Ser	Cys	Gly	
65				70				75								
ggc	cgt	gtc	aac	cgc	tgc	att	cct	cag	ttc	tgg	agg	tgc	gat	ggc	caa	289
Gly	Arg	Val	Asn	Arg	Cys	Ile	Pro	Gln	Phe	Trp	Arg	Cys	Asp	Gly	Gln	
80				85				90								
gtg	gac	tgc	gac	aac	ggc	tca	gac	gag	caa	ggc	tgt	ccc	ccc	aag	acg	337
Val	Asp	Cys	Asp	Asn	Gly	Ser	Asp	Glu	Gln	Gly	Cys	Pro	Pro	Lys	Thr	
95				100				105								
tgc	tcc	cag	gac	gag	ttt	cgc	tgc	cac	gat	ggg	aag	tgc	atc	tct	cgg	385
Cys	Ser	Gln	Asp	Glu	Phe	Arg	Cys	His	Asp	Gly	Lys	Cys	Ile	Ser	Arg	
110				115				120								
cag	ttc	gtc	tgt	gac	tca	gac	cgg	gac	tgc	ttg	gac	ggc	tca	gac	gag	433
Gln	Phe	Val	Cys	Asp	Ser	Asp	Arg	Asp	Cys	Leu	Asp	Gly	Ser	Asp	Glu	
125				130				135				140				

gcc tcc tgc ccg gtg ctc acc tgt ggt ccc gcc agc ttc cag tgc aac	481
Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn	
145 150 155	
agc tcc acc tgc atc ccc cag ctg tgg gcc tgc gac aac gac ccc gac	529
Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp	
160 165 170	
tgc gaa gat ggc tgc gat gag tgg ccg cag cgc tgt agg ggt ctt tac	577
Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr	
175 180 185	
gtg ttc caa ggg gac agt agc ccc tgc tgc gcc ttc gag ttc cac tgc	625
Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys	
190 195 200	
cta agt ggc gag tgc atc cac tcc agc tgg cgc tgt gat ggt ggc ccc	673
Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro	
205 210 215 220	
gac tgc aag gac aaa tct gac gag gaa aac tgc gct gtg gcc acc tgt	721
Asp Cys Lys Asp Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys	
225 230 235	
cgc cct gac gaa ttc cag tgc tct gat gga aac tgc atc cat ggc agc	769
Arg Pro Asp Glu Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser	
240 245 250	
cgg cag tgt gac cgg gaa tat gac tgc aag gac atg agc gat gaa gtt	817
Arg Gln Cys Asp Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val	
255 260 265	
ggc tgc gtt aat glg aca ctc tgc gag gga ccc aac aag ttc aag tgt	865
Gly Cys Val Asn Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys	
270 275 280	

cac agc ggc gaa tgc atc acc ctg gac aaa gtc tgc aac atg gct aga	913
His Ser Gly Glu Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg	
285                      290                      295                      300	
gac tgc cgg gac tgg tca gat gaa ccc atc aaa gag tgc ggg acc aac	961
Asp Cys Arg Asp Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn	
305                      310                      315	
gaa tgc ttg gac aac aac ggc ggc tgt tcc cac gtc tgc aat gac ctt	1009
Glu Cys Leu Asp Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu	
320                      325                      330	
aag atc ggc tac gag tgc ctg tgc ccc gac ggc ttc cag ctg gtg gcc	1057
Lys Ile Gly Tyr Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala	
335                      340                      345	
cag cga aga tgc gaa gat atc gat gag tgt cag gat ccc gac acc tgc	1105
Gln Arg Arg Cys Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys	
350                      355                      360	
agc cag ctc tgc gtg aac ctg gag ggt ggc tac aag tgc cag tgt gag	1153
Ser Gln Leu Cys Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu	
365                      370                      375                      380	
gaa ggc ttc cag ctg gac ccc cac acg aag gcc tgc aag gct gtg ggc	1201
Glu Gly Phe Gln Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly	
385                      390                      395	
tcc atc gcc tac ctc ttc ttc acc aac cgg cac gag gtc agg aag atg	1249
Ser Ile Ala Tyr Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met	
400                      405                      410	
acg ctg gac cgg agc gag tac acc agc ctc atc ccc aac ctg agg aac	1297
Thr Leu Asp Arg Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn	

415	420	425	
gtg gtc gct ctg gac acg gag gtg gcc agc aat aga atc tac tgg tct			1345
Val Val Ala Leu Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser			
430	435	440	
gac ctg tcc cag aga atg atc tgc agc acc cag ctt gac aga gcc cac			1393
Asp Leu Ser Gln Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His			
445	450	455	460
ggc gtc tct tcc tat gac acc gtc atc agc agg gac atc cag gcc ccc			1441
Gly Val Ser Ser Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro			
465	470	475	
gac ggg ctg gct gtg gac tgg atc cac agc aac atc tac tgg acc gac			1489
Asp Gly Leu Ala Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp			
480	485	490	
tct gtc ctg ggc act gtc tct gtt gcg gat acc aag ggc gtg aag agg			1537
Ser Val Leu Gly Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg			
495	500	505	
aaa acg tta ttc agg gag aac ggc tcc aag cca agg gcc atc gtg gtg			1585
Lys Thr Leu Phe Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val			
510	515	520	
gat cct gtt cat ggc ttc atg tac tgg act gac tgg gga act ccc gcc			1633
Asp Pro Val His Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala			
525	530	535	540
aag atc aag aaa ggg ggc ctg aat ggt gtg gac atc tac tcg ctg gtg			1681
Lys Ile Lys Lys Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val			
545	550	555	
act gaa aac att cag tgg ccc aat ggc atc acc cta gat ctc ctc agt			1729
Thr Glu Asn Ile Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser			



560	565	570	
ggc cgc ctc tac tgg gtt gac tcc aaa ctt cac tcc atc tca agc atc	1777		
Gly Arg Leu Tyr Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile			
575	580	585	
gat gtc aat ggg ggc aac cgg aag acc atc ttg gag gat gaa aag agg	1825		
Asp Val Asn Gly Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg			
590	595	600	
ctg gcc cac ccc ttc tcc ttg gcc gtc ttt gag gac aaa gta ttt tgg	1873		
Leu Ala His Pro Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp			
605	610	615	620
aca gat atc atc aac gaa gcc att ttc agt gcc aac cgc ctc aca ggt	1921		
Thr Asp Ile Ile Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly			
625	630	635	
tcc gat gtc aac ttg ttg gct gaa aac cta ctg tcc cca gag gat atg	1969		
Ser Asp Val Asn Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met			
640	645	650	
gtc ctc ttc cac aac ctc acc cag cca aga gga gtg aac tgg tgt gag	2017		
Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu			
655	660	665	
agg acc acc ctg agc aat ggc ggc tgc cag tat ctg tgc ctc cct gcc	2065		
Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala			
670	675	680	
ccg cag atc aac ccc cac tcg ccc aag ttt acc tgc gcc tgc ccg gac	2113		
Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp			
685	690	695	700
ggc atg ctg ctg gcc agg gac atg agg agc tgc ctc aca gag gct gag	2161		

Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu	
705 710 715	
gct gca gtg gcc acc cag gag aca tcc acc gtc agg cta aag gtc agc	2209
Ala Ala Val Ala Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser	
720 725 730	
tcc aca gcc gta agg aca cag cac aca acc acc cgg cct gtt ccc gac	2257
Ser Thr Ala Val Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp	
735 740 745	
acc tcc cgg ctg cct ggg gcc acc cct ggg ctc acc acg gtg gag ata	2305
Thr Ser Arg Leu Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile	
750 755 760	
gtg aca atg tct cac caa gct ctg ggc gac gtt gct ggc aga gga aat	2353
Val Thr Met Ser His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn	
765 770 775 780	
gag aag aag ccc agt agc gtg agg gct ctg tcc att gtc ctc ccc atc	2401
Glu Lys Lys Pro Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile	
785 790 795	
gtg ctc ctc gtc ttc ctt tgc ctg ggg gtc ttc ctt cta tgg aag aac	2449
Val Leu Leu Val Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn	
800 805 810	
tgg cgg ctt aag aac atc aac agc atc aac ttt gac aac ccc gtc tat	2497
Trp Arg Leu Lys Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr	
815 820 825	
cag aag acc aca gag gat gag gtc cac att tgc cac aac cag gac ggc	2545
Gln Lys Thr Thr Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly	
830 835 840	
tac agc tac ccc tcg aga cag atg gtc agt ctg gag gat gac gtg gcg	2593

Tyr Ser Tyr Pro Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala

845                      850                      855                      860

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gtttttatca aagacagaga agaccaaagc attgcctgcc agagcittgt tttatatatt 2713

tattcatctg ggaggcagaa caggcttcgg acagtgccca tgcaatggct tgggttggga 2773

ttttggtttc ttcccttccg gtgaaggata agagaaacag gcccggggcg accaggaatga 2833

cacctccatt tctctccagg aagttttgag tttctctcca cctgacaca atcctcaaac 2893

atggaagatg aaagggcagg ggaatgcagg ccagagaag caagtggcct tcaacacaca 2953

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<210> 22

<211> 860

<212> PRT

<213> Homo sapiens

<400> 22

Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val Ala Leu Leu Leu

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10

15

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Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly		
35	40	45
Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu		
50	55	60
Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn		
65	70	75
Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp		
85	90	95
Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp		
100	105	110
Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys		
115	120	125
Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro		
130	135	140
Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys		
145	150	155
Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly		
165	170	175
Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly		
180	185	190
Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu		
195	200	205
Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp		
210	215	220
Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu		
225	230	235
		240



Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser  
 450 455 460  
 Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala  
 465 470 475 480  
 Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly  
 485 490 495  
 Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe  
 500 505 510  
 Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His  
 515 520 525  
 Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys  
 530 535 540  
 Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile  
 545 550 555 560  
 Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr  
 565 570 575  
 Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly  
 580 585 590  
 Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro  
 595 600 605  
 Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile  
 610 615 620  
 Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn  
 625 630 635 640  
 Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His  
 645 650 655  
 Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu

660	665	670	
Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn			
675	680	685	
Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu			
690	695	700	
Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala			
705	710	715	720
Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val			
725	730	735	
Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu			
740	745	750	
Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser			
755	760	765	
His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro			
770	775	780	
Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val			
785	790	795	800
Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys			
805	810	815	
Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr			
820	825	830	
Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser Tyr Pro			
835	840	845	
Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala			
850	855	860	

<210> 23



<211> 1660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50).. (529)

<400> 23

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Met Leu Leu

1

ctg ttg ctg agt atc atc gtc ctc cac gtc gcg gtg ctg gtg ctg ctg 106

Leu Leu Leu Ser Ile Ile Val Leu His Val Ala Val Leu Val Leu Leu

5

10

15

ttc gtc tcc acg atc gtc agc caa tgg atc gtg ggc aat gga cac gca 154

Phe Val Ser Thr Ile Val Ser Gln Trp Ile Val Gly Asn Gly His Ala

20

25

30

35

act gat ctc tgg cag aac tgt agc acc tct tcc tca gga aat gtc cac 202

Thr Asp Leu Trp Gln Asn Cys Ser Thr Ser Ser Ser Gly Asn Val His

40

45

50

cac tgt ttc tca tca tca cca aac gaa tgg ctg cag tct gtc cag gcc 250

His Cys Phe Ser Ser Ser Pro Asn Glu Trp Leu Gln Ser Val Gln Ala

55

60

65

acc atg atc ctg tgc atc atc ttc agc att ctg tct ctg ttc ctg ttc 298

Thr Met Ile Leu Ser Ile Ile Phe Ser Ile Leu Ser Leu Phe Leu Phe

70

75

80

ttc tgc caa ctc ttc acc ctc acc aag ggg ggc agg ttt tac atc act 346

Phe Cys Gln Leu Phe Thr Leu Thr Lys Gly Gly Arg Phe Tyr Ile Thr  
85 90 95  
gga atc ttc caa att ctt gct ggt ctg tgc gtg atg agt gct gcg gcc 394  
Gly Ile Phe Gln Ile Leu Ala Gly Leu Cys Val Met Ser Ala Ala Ala  
100 105 110 115  
atc tac acg gtg agg cac ccg gag tgg cat ctc acc tcg gat tac tcc 442  
Ile Tyr Thr Val Arg His Pro Glu Trp His Leu Thr Ser Asp Tyr Ser  
120 125 130  
tac ggt ttc gcc tac atc ctg gcc tgg gtg gcc ttc ccc ctg gcc ctt 490  
Tyr Gly Phe Ala Tyr Ile Leu Ala Trp Val Ala Phe Pro Leu Ala Leu  
135 140 145  
ctc agc ggt gtc atc tat gtg atc ttg cgg aaa cgc gaa tgaggcgccc 539  
Leu Ser Gly Val Ile Tyr Val Ile Leu Arg Lys Arg Glu  
150 155 160  
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<210> 24

<211> 160

<212> PRT

<213> Homo sapiens

<400> 24

Met	Leu	Leu	Leu	Leu	Ser	Ile	Ile	Val	Leu	His	Val	Ala	Val	Leu
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Val	Leu	Leu	Phe	Val	Ser	Thr	Ile	Val	Ser	Gln	Trp	Ile	Val	Gly
				20				25					30	Asn
Gly	His	Ala	Thr	Asp	Leu	Trp	Gln	Asn	Cys	Ser	Thr	Ser	Ser	Gly
				35				40					45	
Asn	Val	His	His	Cys	Phe	Ser	Ser	Ser	Pro	Asn	Glu	Trp	Leu	Gln
				50				55					60	Ser
Val	Gln	Ala	Thr	Met	Ile	Leu	Ser	Ile	Ile	Phe	Ser	Ile	Leu	Ser
				65				70					75	Leu
Phe	Leu	Phe	Phe	Cys	Gln	Leu	Phe	Thr	Leu	Thr	Lys	Gly	Gly	Arg
				85				90					95	Phe
Tyr	Ile	Thr	Gly	Ile	Phe	Gln	Ile	Leu	Ala	Gly	Leu	Cys	Val	Met
				100				105					110	Ser
Ala	Ala	Ala	Ile	Tyr	Thr	Val	Arg	His	Pro	Glu	Trp	His	Leu	Thr

115	120	125
Asp Tyr Ser Tyr Gly Phe Ala Tyr Ile Leu Ala Trp Val Ala Phe Pro		
130	135	140
Leu Ala Leu Leu Ser Gly Val Ile Tyr Val Ile Leu Arg Lys Arg Glu		
145	150	155
		160

<210> 25

<211> 3116

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36).. (2717)

<400> 25

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Met Ala Trp Arg Cys Pro

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5

agg atg ggc agg gtc ccg ctg gcc tgg tgc ttg gcg ctg tgc ggc tgg 101

Arg Met Gly Arg Val Pro Leu Ala Trp Cys Leu Ala Leu Cys Gly Trp

10

15

20

gcg tgc atg gcc ccc agg ggc acg cag gct gaa gaa agt ccc ttc gtg 149

Ala Cys Met Ala Pro Arg Gly Thr Gln Ala Glu Glu Ser Pro Phe Val

25

30

35

ggc aac cca ggg aat atc aca ggt gcc cgg gga ctc acg ggc acc ctt 197

Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg Gly Leu Thr Gly Thr Leu

40

45

50

cgg tgt cag ctc cag gtt cag gga gag ccc ccc gag gta cat tgg ctt 245

Arg	Cys	Gln	Leu	Gln	Val	Gln	Gly	Glu	Pro	Pro	Glu	Val	His	Trp	Leu	
55					60					65					70	
cgg	gat	gga	cag	atc	ctg	gag	ctc	gcg	gac	agc	acc	cag	acc	cag	gtg	293
Arg	Asp	Gly	Gln	Ile	Leu	Glu	Leu	Ala	Asp	Ser	Thr	Gln	Thr	Gln	Val	
				75					80					85		
ccc	ctg	ggt	gag	gat	gaa	cag	gat	gac	tgg	ata	gtg	gtc	agc	cag	ctc	341
Pro	Leu	Gly	Glu	Asp	Glu	Gln	Asp	Asp	Trp	Ile	Val	Val	Ser	Gln	Leu	
				90					95					100		
aga	atc	acc	tcc	ctg	cag	ctt	tcc	gac	acg	gga	cag	tac	cag	tgt	ttg	389
Arg	Ile	Thr	Ser	Leu	Gln	Leu	Ser	Asp	Thr	Gly	Gln	Tyr	Gln	Cys	Leu	
				105					110					115		
gtg	ttt	ctg	gga	cat	cag	acc	ttc	gtg	tcc	cag	cct	ggc	tat	gtt	ggg	437
Val	Phe	Leu	Gly	His	Gln	Thr	Phe	Val	Ser	Gln	Pro	Gly	Tyr	Val	Gly	
				120					125					130		
ctg	gag	ggc	ttg	cct	tac	ttc	ctg	gag	gag	ccc	gaa	gac	agg	act	gtg	485
Leu	Glu	Gly	Leu	Pro	Tyr	Phe	Leu	Glu	Glu	Pro	Glu	Asp	Arg	Thr	Val	
135					140					145					150	
gcc	gcc	aac	acc	ccc	ttc	aac	ctg	agc	tgc	caa	gct	cag	gga	ccc	cca	533
Ala	Ala	Asn	Thr	Pro	Phe	Asn	Leu	Ser	Cys	Gln	Ala	Gln	Gly	Pro	Pro	
				155					160					165		
gag	ccc	gtg	gac	cta	ctc	tgg	ctc	cag	gat	gct	gtc	ccc	ctg	gcc	acg	581
Glu	Pro	Val	Asp	Leu	Leu	Trp	Leu	Gln	Asp	Ala	Val	Pro	Leu	Ala	Thr	
				170					175					180		
gct	cca	ggt	cac	ggc	ccc	cag	cgc	agc	ctg	cat	gtt	cca	ggg	ctg	aac	629
Ala	Pro	Gly	His	Gly	Pro	Gln	Arg	Ser	Leu	His	Val	Pro	Gly	Leu	Asn	
				185					190					195		

aag aca tcc tct ttc tcc tgc gaa gcc cat aac gcc aag ggg gtc acc	677
Lys Thr Ser Ser Phe Ser Cys Glu Ala His Asn Ala Lys Gly Val Thr	
200 205 210	
aca tcc cgc aca gcc acc atc aca gtg ctc ccc cag cag ccc cgt aac	725
Thr Ser Arg Thr Ala Thr Ile Thr Val Leu Pro Gln Gln Pro Arg Asn	
215 220 225 230	
ctc cac ctg gtc tcc cgc caa ccc acg gag ctg gag gtg gct tgg act	773
Leu His Leu Val Ser Arg Gln Pro Thr Glu Leu Glu Val Ala Trp Thr	
235 240 245	
cca ggc ctg agc ggc atc tac ccc ctg acc cac tgc acc ctg cag gct	821
Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr His Cys Thr Leu Gln Ala	
250 255 260	
gtg ctg tca gac gat ggg atg ggc atc cag gcg gga gaa cca gac ccc	869
Val Leu Ser Asp Asp Gly Met Gly Ile Gln Ala Gly Glu Pro Asp Pro	
265 270 275	
cca gag gag ccc ctc acc tcg caa gca tcc gtg ccc ccc cat cag ctt	917
Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser Val Pro Pro His Gln Leu	
280 285 290	
cgg cta ggc agc ctc cat cct cac ccc cct tat cac atc cgc gtg gca	965
Arg Leu Gly Ser Leu His Pro His Pro Pro Tyr His Ile Arg Val Ala	
295 300 305 310	
tgc acc agc agc cag ggc ccc tca tcc tgg acc cac tgg ctt cct gtg	1013
Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp Thr His Trp Leu Pro Val	
315 320 325	
gag acg ccg gag gga gtg ccc ctg ggc ccc cct gag aac att agt gct	1061
Glu Thr Pro Glu Gly Val Pro Leu Gly Pro Pro Glu Asn Ile Ser Ala	
330 335 340	

acg cgg aat ggg agc cag gcc ttc gtg cat tgg caa gag ccc cgg gcg	1109
Thr Arg Asn Gly Ser Gln Ala Phe Val His Trp Gln Glu Pro Arg Ala	
345 350 355	
ccc ctg cag ggt acc ctg tta ggg tac cgg ctg gcg tat caa ggc cag	1157
Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg Leu Ala Tyr Gln Gly Gln	
360 365 370	
gac acc cca gag gtg cta atg gac ata ggg cta agg caa gag gtg acc	1205
Asp Thr Pro Glu Val Leu Met Asp Ile Gly Leu Arg Gln Glu Val Thr	
375 380 385 390	
ctg gag ctg cag ggg gac ggg tct gtg tcc aat ctg aca gtg tgt gtg	1253
Leu Glu Leu Gln Gly Asp Gly Ser Val Ser Asn Leu Thr Val Cys Val	
395 400 405	
gca gcc tac act gct gct ggg gat gga ccc tgg agc ctc cca gta ccc	1301
Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro Trp Ser Leu Pro Val Pro	
410 415 420	
ctg gag gcc tgg cgc cca ggg gaa gca cag cca gtc cac cag ctg gtg	1349
Leu Glu Ala Trp Arg Pro Gly Glu Ala Gln Pro Val His Gln Leu Val	
425 430 435	
aag gaa cct tca act cct gcc ttc tcg tgg ccc tgg tgg tat gta ctg	1397
Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp Pro Trp Trp Tyr Val Leu	
440 445 450	
cta gga gca gtc gtg gcc gct gcc tgt gtc ctc atc ttg gct ctc ttc	1445
Leu Gly Ala Val Val Ala Ala Ala Cys Val Leu Ile Leu Ala Leu Phe	
455 460 465 470	
ctt gtc cac cgg cga aag aag gag acc cgt tat gga gaa gtg ttt gaa	1493
Leu Val His Arg Arg Lys Lys Glu Thr Arg Tyr Gly Glu Val Phe Glu	

475	480	485	
cca aca gtg gaa aga ggt gaa ctg gta gtc agg tac cgc gtg cgc aag	1541		
Pro Thr Val Glu Arg Gly Glu Leu Val Val Arg Tyr Arg Val Arg Lys			
490	495	500	
tcc tac agt cgt cgg acc act gaa gct acc ttg aac agc ctg ggc atc	1589		
Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr Leu Asn Ser Leu Gly Ile			
505	510	515	
agt gaa gag ctg aag gag aag ctg cgg gat gtg atg gtg gac cgg cac	1637		
Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp Val Met Val Asp Arg His			
520	525	530	
aag gtg gcc ctg ggg aag act ctg gga gag gga gag ttt gga gct gtg	1685		
Lys Val Ala Leu Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly Ala Val			
535	540	545	550
atg gaa ggc cag ctc aac cag gac gac tcc atc ctc aag gtg gct gtg	1733		
Met Glu Gly Gln Leu Asn Gln Asp Asp Ser Ile Leu Lys Val Ala Val			
555	560	565	
aag acg atg aag att gcc atc tgc acg agg tca gag ctg gag gat ttc	1781		
Lys Thr Met Lys Ile Ala Ile Cys Thr Arg Ser Glu Leu Glu Asp Phe			
570	575	580	
ctg agt gaa gcg gtc tgc atg aag gaa ttt gac cat ccc aac gtc atg	1829		
Leu Ser Glu Ala Val Cys Met Lys Glu Phe Asp His Pro Asn Val Met			
585	590	595	
agg ctc atc ggt gtc tgt ttc cag ggt tct gaa cga gag agc ttc cca	1877		
Arg Leu Ile Gly Val Cys Phe Gln Gly Ser Glu Arg Glu Ser Phe Pro			
600	605	610	
gca cct gtg gtc atc tta cct ttc atg aaa cat gga gac cta cac agc	1925		
Ala Pro Val Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ser			



615	620	625	630	
ttc ctc ctc tat tcc cgg ctc ggg ggc cag cca gtg tac ctg ccc act				1973
Phe Leu Leu Tyr Ser Arg Leu Gly Gly Gln Pro Val Tyr Leu Pro Thr				
	635	640	645	
cag atg cta gtg aag ttc atg gca gac atc gcc agt ggc atg gag tat				2021
Gln Met Leu Val Lys Phe Met Ala Asp Ile Ala Ser Gly Met Glu Tyr				
	650	655	660	
ctg agt acc aag aga ttc ata cac cgg gac ctg gcg gcc agg aac tgc				2069
Leu Ser Thr Lys Arg Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys				
	665	670	675	
atg ctg aat gag aac atg tcc gtg tgt gtg gcg gac ttc ggg ctc tcc				2117
Met Leu Asn Glu Asn Met Ser Val Cys Val Ala Asp Phe Gly Leu Ser				
	680	685	690	
aag aag atc tac aat ggg gac tac tac cgc cag gga cgt atc gcc aag				2165
Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys				
695	700	705	710	
atg cca gtc aag tgg att gcc att gag agt cta gct gac cgt gtc tac				2213
Met Pro Val Lys Trp Ile Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr				
	715	720	725	
acc agc aag agc gat gtg tgg tcc ttc ggg gtg aca atg tgg gag att				2261
Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Thr Met Trp Glu Ile				
	730	735	740	
gcc aca aga ggc caa acc cca tat ccg ggc gtg gag aac agc gag att				2309
Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile				
	745	750	755	
tat gac tat ctg cgc cag gga aat cgc ctg aag cag cct gcg gac tgt				2357

Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys  
 760 765 770  
 ctg gat gga ctg tat gcc ttg atg tcg cgg tgc tgg gag cta aat ccc 2405  
 Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg Cys Trp Glu Leu Asn Pro  
 775 780 785 790  
 cag gac cgg cca agt ttt aca gag ctg cgg gaa gat ttg gag aac aca 2453  
 Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr  
 795 800 805  
 ctg aag gcc ttg cct cct gcc cag gag cct gac gaa atc ctc tat gtc 2501  
 Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val  
 810 815 820  
 aac atg gat gag ggt gga ggt tat cct gaa ccc cct gga gct gca gga 2549  
 Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly  
 825 830 835  
 gga gct gac ccc cca acc cag cca gac cct aag gat tcc tgt agc tgc 2597  
 Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys  
 840 845 850  
 ctc act gcg gct gag gtc cat cct gct gga cgc tat gtc ctc tgc cct 2645  
 Leu Thr Ala Ala Glu Val His Pro Ala Gly Arg Tyr Val Leu Cys Pro  
 855 860 865 870  
 tcc aca acc cct agc ccc gct cag cct gct gat agg ggc tcc cca gca 2693  
 Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala  
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 gcc cca ggg cag gag gat ggt gcc tgagacaacc ctccacctgg tactccctct 2747  
 Ala Pro Gly Gln Glu Asp Gly Ala  
 890  
 caggatccaa gctaagcact gccactgggg gaaactccac ctccacctt tcccaccca 2807

cgcccttatcc ccacttgcag cccgtgtcttc ctacctatcc cacctccatc ccagacaggt 2867  
cccctggccit ctctgtgcag tagcatcacc ttgaaagcag tagcatcacc atctgtaaaa 2927  
ggaaggggtt ggattgcaat atctgaagcc ctcccaggig ttaacattcc aagactctag 2987  
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<210> 26

<211> 894

<212> PRT

<213> Homo sapiens

<400> 26

Met	Ala	Trp	Arg	Cys	Pro	Arg	Met	Gly	Arg	Val	Pro	Leu	Ala	Trp	Cys
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Leu	Ala	Leu	Cys	Gly	Trp	Ala	Cys	Met	Ala	Pro	Arg	Gly	Thr	Gln	Ala
				20				25					30		
Glu	Glu	Ser	Pro	Phe	Val	Gly	Asn	Pro	Gly	Asn	Ile	Thr	Gly	Ala	Arg
				35				40					45		
Gly	Leu	Thr	Gly	Thr	Leu	Arg	Cys	Gln	Leu	Gln	Val	Gln	Gly	Glu	Pro
				50				55					60		
Pro	Glu	Val	His	Trp	Leu	Arg	Asp	Gly	Gln	Ile	Leu	Glu	Leu	Ala	Asp
				65				70					75		80
Ser	Thr	Gln	Thr	Gln	Val	Pro	Leu	Gly	Glu	Asp	Glu	Gln	Asp	Asp	Trp
				85				90					95		
Ile	Val	Val	Ser	Gln	Leu	Arg	Ile	Thr	Ser	Leu	Gln	Leu	Ser	Asp	Thr
				100				105					110		
Gly	Gln	Tyr	Gln	Cys	Leu	Val	Phe	Leu	Gly	His	Gln	Thr	Phe	Val	Ser

115	120	125			
Gln	Pro	Gly	Tyr	Val	Gly
		Leu	Glu	Gly	Leu
			Pro	Tyr	Phe
				Leu	Glu
				Glu	
130	135	140			
Pro	Glu	Asp	Arg	Thr	Val
		Ala	Ala	Asn	Thr
			Pro	Phe	Asn
				Leu	Ser
				Cys	
145	150	155	160		
Gln	Ala	Gln	Gly	Pro	Pro
		Glu	Pro	Val	Asp
			Leu	Leu	Trp
				Leu	Gln
				Asp	
165	170	175			
Ala	Val	Pro	Leu	Ala	Thr
		Ala	Pro	Gly	His
			Gly	Pro	Gln
				Arg	Ser
				Leu	
180	185	190			
His	Val	Pro	Gly	Leu	Asn
		Lys	Thr	Ser	Ser
			Phe	Ser	Cys
				Glu	Ala
				His	
195	200	205			
Asn	Ala	Lys	Gly	Val	Thr
		Thr	Ser	Arg	Thr
			Ala	Thr	Ile
				Thr	Val
				Leu	
210	215	220			
Pro	Gln	Gln	Pro	Arg	Asn
		Leu	His	Leu	Val
			Ser	Arg	Gln
				Pro	Thr
				Glu	
225	230	235	240		
Leu	Glu	Val	Ala	Trp	Thr
		Pro	Gly	Leu	Ser
			Gly	Ile	Tyr
				Pro	Leu
				Thr	
245	250	255			
His	Cys	Thr	Leu	Gln	Ala
		Val	Leu	Ser	Asp
			Asp	Gly	Met
				Gly	Ile
				Gln	
260	265	270			
Ala	Gly	Glu	Pro	Asp	Pro
		Pro	Glu	Glu	Pro
			Leu	Thr	Ser
				Gln	Ala
				Ser	
275	280	285			
Val	Pro	Pro	His	Gln	Leu
		Arg	Leu	Gly	Ser
			Leu	His	Pro
				His	Pro
				Pro	
290	295	300			
Tyr	His	Ile	Arg	Val	Ala
		Cys	Thr	Ser	Ser
			Gln	Gly	Pro
				Ser	Ser
				Trp	
305	310	315	320		
Thr	His	Trp	Leu	Pro	Val
		Glu	Thr	Pro	Glu
			Gly	Val	Pro
				Leu	Gly
				Pro	

325	330	335	
Pro Glu Asn Ile Ser Ala Thr Arg Asn Gly Ser Gln Ala Phe Val His			
340	345	350	
Trp Gln Glu Pro Arg Ala Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg			
355	360	365	
Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly			
370	375	380	
Leu Arg Gln Glu Val Thr Leu Glu Leu Gln Gly Asp Gly Ser Val Ser			
385	390	395	400
Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro			
405	410	415	
Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Gly Glu Ala Gln			
420	425	430	
Pro Val His Gln Leu Val Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp			
435	440	445	
Pro Trp Trp Tyr Val Leu Leu Gly Ala Val Val Ala Ala Ala Cys Val			
450	455	460	
Leu Ile Leu Ala Leu Phe Leu Val His Arg Arg Lys Lys Glu Thr Arg			
465	470	475	480
Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly Glu Leu Val Val			
485	490	495	
Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr			
500	505	510	
Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp			
515	520	525	
Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys Thr Leu Gly Glu			
530	535	540	

Gly	Glu	Phe	Gly	Ala	Val	Met	Glu	Gly	Gln	Leu	Asn	Gln	Asp	Asp	Ser
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Ile	Leu	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	Ile	Ala	Ile	Cys	Thr	Arg
				565					570					575	
Ser	Glu	Leu	Glu	Asp	Phe	Leu	Ser	Glu	Ala	Val	Cys	Met	Lys	Glu	Phe
			580						585					590	
Asp	His	Pro	Asn	Val	Met	Arg	Leu	Ile	Gly	Val	Cys	Phe	Gln	Gly	Ser
			595				600						605		
Glu	Arg	Glu	Ser	Phe	Pro	Ala	Pro	Val	Val	Ile	Leu	Pro	Phe	Met	Lys
	610					615						620			
His	Gly	Asp	Leu	His	Ser	Phe	Leu	Leu	Tyr	Ser	Arg	Leu	Gly	Gly	Gln
625					630					635					640
Pro	Val	Tyr	Leu	Pro	Thr	Gln	Met	Leu	Val	Lys	Phe	Met	Ala	Asp	Ile
					645					650				655	
Ala	Ser	Gly	Met	Glu	Tyr	Leu	Ser	Thr	Lys	Arg	Phe	Ile	His	Arg	Asp
			660						665					670	
Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Asn	Glu	Asn	Met	Ser	Val	Cys	Val
			675						680					685	
Ala	Asp	Phe	Gly	Leu	Ser	Lys	Lys	Ile	Tyr	Asn	Gly	Asp	Tyr	Tyr	Arg
	690					695							700		
Gln	Gly	Arg	Ile	Ala	Lys	Met	Pro	Val	Lys	Trp	Ile	Ala	Ile	Glu	Ser
705					710						715				720
Leu	Ala	Asp	Arg	Val	Tyr	Thr	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly
					725						730			735	
Val	Thr	Met	Trp	Glu	Ile	Ala	Thr	Arg	Gly	Gln	Thr	Pro	Tyr	Pro	Gly
				740						745				750	

Val	Glu	Asn	Ser	Glu	Ile	Tyr	Asp	Tyr	Leu	Arg	Gln	Gly	Asn	Arg	Leu
	755						760					765			
Lys	Gln	Pro	Ala	Asp	Cys	Leu	Asp	Gly	Leu	Tyr	Ala	Leu	Met	Ser	Arg
	770						775					780			
Cys	Trp	Glu	Leu	Asn	Pro	Gln	Asp	Arg	Pro	Ser	Phe	Thr	Glu	Leu	Arg
785							790					795			800
Glu	Asp	Leu	Glu	Asn	Thr	Leu	Lys	Ala	Leu	Pro	Pro	Ala	Gln	Glu	Pro
							805					810			815
Asp	Glu	Ile	Leu	Tyr	Val	Asn	Met	Asp	Glu	Gly	Gly	Gly	Tyr	Pro	Glu
							820					825			830
Pro	Pro	Gly	Ala	Ala	Gly	Gly	Ala	Asp	Pro	Pro	Thr	Gln	Pro	Asp	Pro
							835					840			845
Lys	Asp	Ser	Cys	Ser	Cys	Leu	Thr	Ala	Ala	Glu	Val	His	Pro	Ala	Gly
							850					855			860
Arg	Tyr	Val	Leu	Cys	Pro	Ser	Thr	Thr	Pro	Ser	Pro	Ala	Gln	Pro	Ala
865							870					875			880
Asp	Arg	Gly	Ser	Pro	Ala	Ala	Pro	Gly	Gln	Glu	Asp	Gly	Ala		
							885					890			

<210> 27

<211> 3781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (4).. (2994)

<400> 27

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ttc ggc gtc aac gag agt acg ggg ctg agc ctg gaa cag gtc aag aag	96
Phe Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys	
20 25 30	
ctt aag gag aga tgg ggc tcc aac gag tta ccg gct gaa gaa gga aaa	144
Leu Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys	
35 40 45	
acc tlg ctg gaa ctt gtg att gag cag ttt gaa gac tlg cta gtt agg	192
Thr Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg	
50 55 60	
att tta tta ctg gca gca tgt ata tct ttt gtt ttg gct tgg ttt gaa	240
Ile Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu	
65 70 75	
gaa ggt gaa gaa aca att aca gcc ttt gta gaa cct ttt gta att tta	288
Glu Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu	
80 85 90 95	
ctc ata tta gta gcc aat gca att gtg ggt gta tgg cag gaa aga aat	336
Leu Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn	
100 105 110	
gct gaa aat gcc atc gaa gcc ctt aag gaa tat gag cct gaa atg ggc	384
Ala Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly	
115 120 125	
aaa gtg tat cga cag gac aga aag agt gtg cag cgg att aaa gct aaa	432
Lys Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys	
130 135 140	



gac ata gtt cct ggt gat att gta gaa att gct gtt ggt gac aaa gtt	480
Asp Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val	
145 150 155	
cct gct gat ata agg tta act tcc atc aaa tct acc aca cta aga gtt	528
Pro Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val	
160 165 170 175	
gac cag tca att ctc aca ggt gaa tct gtc tct gtc atc aag cac act	576
Asp Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr	
180 185 190	
gat ccc gtc cct gac cca cga gct gtc aac caa gat aaa aag aac atg	624
Asp Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met	
195 200 205	
ctg ttt tct ggt aca aac att gct gct ggg aaa gct atg gga gtg gtg	672
Leu Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val	
210 215 220	
gta gca act gga gtt aac acc gaa att ggc aag atc cgg gat gaa atg	720
Val Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met	
225 230 235	
gtg gca aca gaa cag gag aga aca ccc ctt cag caa aaa cta gat gaa	768
Val Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu	
240 245 250 255	
ttt ggg gaa cag ctt tcc aaa gtc atc tcc ctt att tgc att gca gtc	816
Phe Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val	
260 265 270	
tgg atc ata aat att ggg cac ttc aat gac ccg gtt cat gga ggg tcc	864
Trp Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser	

275	280	285	
tgg atc aga ggt gct att tac tac ttt aaa att gca gtg gcc ctg gct	912		
Trp Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala			
290	295	300	
gta gca gcc att cct gaa ggt ctg cct gca gtc atc acc acc tgc ctg	960		
Val Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu			
305	310	315	
gct ctt gga act cgc aga atg gca aag aaa aat gcc att gtt cga agc	1008		
Ala Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser			
320	325	330	335
ctc ccg tct gtg gaa acc ctt ggt tgt act tct gtt atc tgc tca gac	1056		
Leu Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp			
340	345	350	
aag act ggt aca ctt aca aca aac cag atg tca gtc tgc agg atg ttc	1104		
Lys Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe			
355	360	365	
att ctg gac aga gtg gaa ggt gat act tgt tcc ctt aat gag ttt acc	1152		
Ile Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr			
370	375	380	
ata act gga tca act tat gca cct att gga gaa gtg cat aaa gat gat	1200		
Ile Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp			
385	390	395	
aaa cca gtg aat tgt cac cag tat gat ggt ctg gta gaa tta gca aca	1248		
Lys Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr			
400	405	410	415
att tgt gct ctt tgt aat gac tct gct ttg gat tac aat gag gca aag	1296		
Ile Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys			

420	425	430	
ggt gtg tat gaa aaa gtt gga gaa gct aca gag act gct ctc act tgc			1344
Gly Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys			
435	440	445	
cta gta gag aag atg aat gta ttt gat acc gaa ttg aag ggt ctt tct			1392
Leu Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser			
450	455	460	
aaa ata gaa cgt gca aat gcc tgc aac tca gtc att aaa cag ctg atg			1440
Lys Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met			
465	470	475	
aaa aag gaa ttc act cta gag ttt tca cgt gac aga aag tca atg tgc			1488
Lys Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser			
480	485	490	495
gtt tac tgt aca cca aat aaa cca agc agg aca tca atg agc aag atg			1536
Val Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met			
500	505	510	
ttt gtg aag ggt gct cct gaa ggt gtc att gac agg tgc acc cac att			1584
Phe Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile			
515	520	525	
cga gtt gga agt act aag gtt cct atg acc tct gga gtc aaa cag aag			1632
Arg Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys			
530	535	540	
atc atg tct gtc att cga gag tgg ggt agt ggc agc gac aca ctg cga			1680
Ile Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg			
545	550	555	
tgc ctg gcc ctg gcc act cat gac aac cca ctg aga aga gaa gaa atg			1728

Cys	Leu	Ala	Leu	Ala	Thr	His	Asp	Asn	Pro	Leu	Arg	Arg	Glu	Glu	Met		
560					565					570					575		
cac	ctt	gag	gac	tct	gcc	aac	ttt	att	aaa	tat	gag	acc	aat	ctg	acc	1776	
His	Leu	Glu	Asp	Ser	Ala	Asn	Phe	Ile	Lys	Tyr	Glu	Thr	Asn	Leu	Thr		
				580						585					590		
ttc	gtt	ggc	tgc	gtg	ggc	atg	ctg	gat	cct	ccg	aga	atc	gag	gtg	gcc	1824	
Phe	Val	Gly	Cys	Val	Gly	Met	Leu	Asp	Pro	Pro	Arg	Ile	Glu	Val	Ala		
				595						600					605		
tcc	tcc	gtg	aag	ctg	tgc	cgg	caa	gca	ggc	atc	cgg	gtc	atc	atg	atc	1872	
Ser	Ser	Val	Lys	Leu	Cys	Arg	Gln	Ala	Gly	Ile	Arg	Val	Ile	Met	Ile		
				610						615					620		
act	ggg	gac	aac	aag	ggc	act	gct	gtg	gcc	atc	tgt	cgc	cgc	atc	ggc	1920	
Thr	Gly	Asp	Asn	Lys	Gly	Thr	Ala	Val	Ala	Ile	Cys	Arg	Arg	Ile	Gly		
				625						630					635		
atc	ttc	ggg	cag	gat	gag	gac	gtg	acg	tca	aaa	gct	ttc	aca	ggc	cgg	1968	
Ile	Phe	Gly	Gln	Asp	Glu	Asp	Val	Thr	Ser	Lys	Ala	Phe	Thr	Gly	Arg		
640					645						650				655		
gag	ttt	gat	gaa	ctc	aac	ccc	tcc	gcc	cag	cga	gac	gcc	tgc	ctg	aac	2016	
Glu	Phe	Asp	Glu	Leu	Asn	Pro	Ser	Ala	Gln	Arg	Asp	Ala	Cys	Leu	Asn		
					660						665				670		
gcc	cgc	tgt	ttt	gct	cga	gtt	gaa	ccc	tcc	cac	aag	tct	aaa	atc	gtt	2064	
Ala	Arg	Cys	Phe	Ala	Arg	Val	Glu	Pro	Ser	His	Lys	Ser	Lys	Ile	Val		
				675							680				685		
gaa	ttt	ctt	cag	tct	ttt	gat	gag	att	aca	gct	atg	act	ggc	gat	ggc	2112	
Glu	Phe	Leu	Gln	Ser	Phe	Asp	Glu	Ile	Thr	Ala	Met	Thr	Gly	Asp	Gly		
				690							695				700		
gtg	aac	gat	gct	cct	gct	ctg	aag	aaa	gcc	gag	att	ggc	att	gct	atg	2160	

Val	Asn	Asp	Ala	Pro	Ala	Leu	Lys	Lys	Ala	Glu	Ile	Gly	Ile	Ala	Met	
705				710				715								
ggc	tct	ggc	act	gcg	gtg	gct	aaa	acc	gcc	tct	gag	atg	gtc	ctg	gcg	2208
Gly	Ser	Gly	Thr	Ala	Val	Ala	Lys	Thr	Ala	Ser	Glu	Met	Val	Leu	Ala	
720				725				730				735				
gat	gac	aac	ttc	tcc	acc	att	gtg	gct	gcc	gtt	gag	gag	ggg	cgg	gca	2256
Asp	Asp	Asn	Phe	Ser	Thr	Ile	Val	Ala	Ala	Val	Glu	Glu	Gly	Arg	Ala	
740				745				750								
atc	tac	aac	aac	atg	aaa	cag	ttc	atc	cgc	tac	ctc	atc	tcg	tcc	aac	2304
Ile	Tyr	Asn	Asn	Met	Lys	Gln	Phe	Ile	Arg	Tyr	Leu	Ile	Ser	Ser	Asn	
755				760				765								
gtc	ggg	gaa	gtt	gtc	tgt	att	ttc	ctg	aca	gca	gcc	ctt	gga	ttt	ccc	2352
Val	Gly	Glu	Val	Val	Cys	Ile	Phe	Leu	Thr	Ala	Ala	Leu	Gly	Phe	Pro	
770				775				780								
gag	gct	ttg	att	cct	gtt	cag	ctg	ctc	tgg	gtc	aat	ctg	gtg	aca	gat	2400
Glu	Ala	Leu	Ile	Pro	Val	Gln	Leu	Leu	Trp	Val	Asn	Leu	Val	Thr	Asp	
785				790				795								
ggc	ctg	cct	gcc	act	gca	ctg	ggg	ttc	aac	cct	cct	gat	ctg	gac	atc	2448
Gly	Leu	Pro	Ala	Thr	Ala	Leu	Gly	Phe	Asn	Pro	Pro	Asp	Leu	Asp	Ile	
800				805				810				815				
atg	aat	aaa	cct	ccc	cgg	aac	cca	aag	gaa	cca	ttg	atc	agc	ggg	tgg	2496
Met	Asn	Lys	Pro	Pro	Arg	Asn	Pro	Lys	Glu	Pro	Leu	Ile	Ser	Gly	Trp	
820				825				830								
ctc	ttt	ttc	cgt	tac	ttg	gct	att	ggc	tgt	tac	gtc	ggc	gct	gct	acc	2544
Leu	Phe	Phe	Arg	Tyr	Leu	Ala	Ile	Gly	Cys	Tyr	Val	Gly	Ala	Ala	Thr	
835				840				845								

gtg ggt gct gct gca tgg tgg ttc att gct gct gac ggt ggt cca aga	2592
Val Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg	
850 855 860	
gtg tcc ttc tac cag ctg agt cat ttc cta cag tgt aaa gag gac aac	2640
Val Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn	
865 870 875	
ccg gac ttt gaa ggc gtg gat tgt gca atc ttt gaa tcc cca tac ccg	2688
Pro Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro	
880 885 890 895	
atg aca atg gcg ctc tct gtt cta gta act ata gaa atg tgt aac gcc	2736
Met Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala	
900 905 910	
ctc aac agc ttg tcc gaa aac cag tcc ttg ctg agg atg ccc ccc tgg	2784
Leu Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp	
915 920 925	
gag aac atc tgg ctc gtg ggc tcc atc tgc ctg tcc atg tca ctc cac	2832
Glu Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His	
930 935 940	
ttc ctg atc ctc tat gtc gaa ccc ttg cca ctc atc ttc cag atc aca	2880
Phe Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr	
945 950 955	
ccg ctg aac gtg acc cag tgg ctg atg gtg ctg aaa atc tcc ttg ccc	2928
Pro Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro	
960 965 970 975	
gtg att ctc atg gat gag acg ctc aag ttt gtg gcc cgc aac tac ctg	2976
Val Ile Leu Met Asp Glu Thr Leu Lys Phe Val Ala Arg Asn Tyr Leu	
980 985 990	

gaa cct gca ata ctg gag taaccgcttc ctaaaccatt ttgcagaaat 3024

Glu Pro Ala Ile Leu Glu

995

gtaaggggtgt tcggttgcgt gcatgtgcgt ttttagcaac acatctacca accctgtgca 3084

tgactgaigt tggggaaaaa gaaaagtaaa aaacttccca actcactttg tgttatgttg 3144

aggaaatgtg tattaccaat ggggttgta gcttttaaat caaaatactg attacagatg 3204

tacaatttag cttaatcaga aagcctctcc agagaagttt ggtttctttg ctgcaagagg 3264

aatgaggctc tgtaacctta tctaagaact tggaagccgt cagccaagtc gccacatttc 3324

ctgcaaaat gtcatagctt atataaaigt acagtattca attgtaatgc atgcttcggt 3384

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aggcctccag ttcatittca gttattttct gagtgtgcag acagctatit cgcactgtat 3564

taaagtiaac ttattttaatg aaatcagaag cagtagacag atgttggatc aatacaaata 3624

ttgtgatgca tttatcttaa taaaatgcta aatgtcaatt tatcactgcg catgtttgac 3684

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cagacatggc ttcaggtaaa taaatctatt ctatgat 3781

<210> 28

<211> 997

<212> PRT

<213> Homo sapiens

<400> 28

Met Glu Asn Ala His Thr Lys Thr Val Glu Glu Val Leu Gly His Phe

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Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys Leu

20 25 30

Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys Thr

35	40	45	
Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile			
50	55	60	
Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu			
65	70	75	80
Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu			
85	90	95	
Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala			
100	105	110	
Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys			
115	120	125	
Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp			
130	135	140	
Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro			
145	150	155	160
Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp			
165	170	175	
Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp			
180	185	190	
Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu			
195	200	205	
Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val			
210	215	220	
Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val			
225	230	235	240
Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe			



245	250	255	
Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp			
260	265	270	
Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp			
275	280	285	
Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val			
290	295	300	
Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala			
305	310	315	320
Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu			
325	330	335	
Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys			
340	345	350	
Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile			
355	360	365	
Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr Ile			
370	375	380	
Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp Lys			
385	390	395	400
Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile			
405	410	415	
Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys Gly			
420	425	430	
Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys Leu			
435	440	445	
Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser Lys			
450	455	460	

Ile	Glu	Arg	Ala	Asn	Ala	Cys	Asn	Ser	Val	Ile	Lys	Gln	Leu	Met	Lys
465				470						475					480
Lys	Glu	Phe	Thr	Leu	Glu	Phe	Ser	Arg	Asp	Arg	Lys	Ser	Met	Ser	Val
				485						490					495
Tyr	Cys	Thr	Pro	Asn	Lys	Pro	Ser	Arg	Thr	Ser	Met	Ser	Lys	Met	Phe
				500						505					510
Val	Lys	Gly	Ala	Pro	Glu	Gly	Val	Ile	Asp	Arg	Cys	Thr	His	Ile	Arg
				515						520					525
Val	Gly	Ser	Thr	Lys	Val	Pro	Met	Thr	Ser	Gly	Val	Lys	Gln	Lys	Ile
				530						535					540
Met	Ser	Val	Ile	Arg	Glu	Trp	Gly	Ser	Gly	Ser	Asp	Thr	Leu	Arg	Cys
545					550						555				560
Leu	Ala	Leu	Ala	Thr	His	Asp	Asn	Pro	Leu	Arg	Arg	Glu	Glu	Met	His
					565						570				575
Leu	Glu	Asp	Ser	Ala	Asn	Phe	Ile	Lys	Tyr	Glu	Thr	Asn	Leu	Thr	Phe
				580							585				590
Val	Gly	Cys	Val	Gly	Met	Leu	Asp	Pro	Pro	Arg	Ile	Glu	Val	Ala	Ser
				595							600				605
Ser	Val	Lys	Leu	Cys	Arg	Gln	Ala	Gly	Ile	Arg	Val	Ile	Met	Ile	Thr
				610							615				620
Gly	Asp	Asn	Lys	Gly	Thr	Ala	Val	Ala	Ile	Cys	Arg	Arg	Ile	Gly	Ile
625					630						635				640
Phe	Gly	Gln	Asp	Glu	Asp	Val	Thr	Ser	Lys	Ala	Phe	Thr	Gly	Arg	Glu
					645						650				655
Phe	Asp	Glu	Leu	Asn	Pro	Ser	Ala	Gln	Arg	Asp	Ala	Cys	Leu	Asn	Ala
				660							665				670

Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu  
 675 680 685  
 Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val  
 690 695 700  
 Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly  
 705 710 715 720  
 Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp  
 725 730 735  
 Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile  
 740 745 750  
 Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val  
 755 760 765  
 Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu  
 770 775 780  
 Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp Gly  
 785 790 795 800  
 Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile Met  
 805 810 815  
 Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu  
 820 825 830  
 Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val  
 835 840 845  
 Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val  
 850 855 860  
 Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro  
 865 870 875 880  
 Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro Met

885	890	895
Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu		
900	905	910
Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp Glu		
915	920	925
Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe		
930	935	940
Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro		
945	950	955
Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro Val		960
965	970	975
Ile Leu Met Asp Glu Thr Leu Lys Phe Val Ala Arg Asn Tyr Leu Glu		
980	985	990
Pro Ala Ile Leu Glu		
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<210> 29

<211> 1103

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133).. (834)

<400> 29

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ggctcctgac ca atg ggg aag tgg cat gtg gga ggg cgc cgg ggt tcc ccc 171



aat gag gta tca aag cct ctg gcc cac cac atc cct gtg gag aag atc 603  
Asn Glu Val Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile  
145 150 155  
tgt gag aag ctt aag aag aag gac agc cag ata tgt gag ctt aag tat 651  
Cys Glu Lys Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr  
160 165 170  
gac aag cag atc gac ctg agc aca gtg gac ctg aag aag ctc cga gtt 699  
Asp Lys Gln Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val  
175 180 185  
aaa gag ctg aag aag att ctg gat gac tgg ggg gag aca tgc aaa ggc 747  
Lys Glu Leu Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly  
190 195 200 205  
tgt gca gaa aag tct gac tac atc cgg aag ata aat gaa ctg atg cct 795  
Cys Ala Glu Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro  
210 215 220  
aaa tat gcc ccc aag gca gcc agt gca ccg acc gat ttg tagtctgctc 844  
Lys Tyr Ala Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu  
225 230  
aatctctgtt gcacctgagg gggaaaaaac agttcaactg cttactccca aaacagcctt 904  
tttgtaattt attttttaag tgggctcctg acaatactgt atcagatgtg aagcctggag 964  
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<210> 30

<211> 234

<212> PRT

<213> Homo sapiens

<400> 30

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Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg Arg Arg Arg

35 40 45

Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly Leu Ala Val

50 55 60

Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu Arg Pro Gly

65 70 75 80

Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr Gln Asp Leu

85 90 95

Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu Asn Glu Leu

100 105 110

Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg Leu Cys Tyr

115 120 125

Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile Asn Glu Val

130 135 140

Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile Cys Glu Lys

145 150 155 160

Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr Asp Lys Gln

165 170 175

Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val Lys Glu Leu

180 185 190

Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly Cys Ala Glu

195	200	205	
Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro Lys Tyr Ala			
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Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu			
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Met Glu Ser Glu Thr Glu Pro			
1 5			
gag ccc gtc acg ctc ctg gtg aag agc ccc aac cag cgc cac cgc gac 162			
Glu Pro Val Thr Leu Leu Val Lys Ser Pro Asn Gln Arg His Arg Asp			
10 15 20			
ttg gag ctg agt ggc gac cgc ggc tgg agt gtg ggc cac ctc aag gcc 210			
Leu Glu Leu Ser Gly Asp Arg Gly Trp Ser Val Gly His Leu Lys Ala			
25 30 35			
cac ctg agc cgc gtc tac ccc gag cgt ccg cgt cca gag gac cag agg 258			
His Leu Ser Arg Val Tyr Pro Glu Arg Pro Arg Pro Glu Asp Gln Arg			
40 45 50 55			



tta att tat tct ggg aag ctg ttg ttg gat cac caa tgt ctc agg gac	306
Leu Ile Tyr Ser Gly Lys Leu Leu Leu Asp His Gln Cys Leu Arg Asp	
60 65 70	
ttg ctt cca aag cag gaa aaa cgg cat gtt ttg cat ctg gtg tgc aat	354
Leu Leu Pro Lys Gln Glu Lys Arg His Val Leu His Leu Val Cys Asn	
75 80 85	
gtg aag agt cct tca aaa atg cca gaa atc aac gcc aag gtg gct gaa	402
Val Lys Ser Pro Ser Lys Met Pro Glu Ile Asn Ala Lys Val Ala Glu	
90 95 100	
tcc aca gag gag cct gct ggt tct aat cgg gga cag tat cct gag gat	450
Ser Thr Glu Glu Pro Ala Gly Ser Asn Arg Gly Gln Tyr Pro Glu Asp	
105 110 115	
tcc tca agt gat ggt tta agg caa agg gaa gtt ctt cgg aac ctt tct	498
Ser Ser Ser Asp Gly Leu Arg Gln Arg Glu Val Leu Arg Asn Leu Ser	
120 125 130 135	
tcc cct gga tgg gaa aac atc tca agg cct gaa gct gcc cag cag gca	546
Ser Pro Gly Trp Glu Asn Ile Ser Arg Pro Glu Ala Ala Gln Gln Ala	
140 145 150	
ttc caa ggc ctg ggt cct ggt ttc tcc ggt tac aca ccc tat ggg tgg	594
Phe Gln Gly Leu Gly Pro Gly Phe Ser Gly Tyr Thr Pro Tyr Gly Trp	
155 160 165	
ctt cag ctt tcc tgg ttc cag cag ata tat gca cga cag tac tac atg	642
Leu Gln Leu Ser Trp Phe Gln Gln Ile Tyr Ala Arg Gln Tyr Tyr Met	
170 175 180	
caa tat tta gca gcc act gct gca tca ggg gct ttt gtt cca cca cca	690
Gln Tyr Leu Ala Ala Thr Ala Ala Ser Gly Ala Phe Val Pro Pro Pro	

185	190	195	
agt gca caa gag ata cct gtg gtc tct gca cct gct cca gcc cct att	738		
Ser Ala Gln Glu Ile Pro Val Val Ser Ala Pro Ala Pro Ala Pro Ile			
200	205	210	215
cac aac cag ttt cca gct gaa aac cag cct gcc aat cag aat gct gct	786		
His Asn Gln Phe Pro Ala Glu Asn Gln Pro Ala Asn Gln Asn Ala Ala			
220	225	230	
cct caa gtg gtt gtt aat cct gga gcc aat caa aat ttg cgg atg aat	834		
Pro Gln Val Val Val Asn Pro Gly Ala Asn Gln Asn Leu Arg Met Asn			
235	240	245	
gca caa ggt ggc cct att gtg gaa gaa gat gat gaa ata aat cga gat	882		
Ala Gln Gly Gly Pro Ile Val Glu Glu Asp Asp Glu Ile Asn Arg Asp			
250	255	260	
tgg ttg gat tgg acc tat tca gca gct aca ttt tct gtt ttt ctc agt	930		
Trp Leu Asp Trp Thr Tyr Ser Ala Ala Thr Phe Ser Val Phe Leu Ser			
265	270	275	
atc ctc tac ttc tac tcc tcc ctg agc aga ttc ctc atg gtc atg ggg	978		
Ile Leu Tyr Phe Tyr Ser Ser Leu Ser Arg Phe Leu Met Val Met Gly			
280	285	290	295
gcc acc gtt gtt atg tac ctg cat cac gtt ggg tgg ttt cca ttt aga	1026		
Ala Thr Val Val Met Tyr Leu His His Val Gly Trp Phe Pro Phe Arg			
300	305	310	
ccg agg ccg gtt cag aac ttc cca aat gat ggt cct cct cct gac gtt	1074		
Pro Arg Pro Val Gln Asn Phe Pro Asn Asp Gly Pro Pro Pro Asp Val			
315	320	325	
gta aat cag gac ccc aac aat aac tta cag gaa ggc act gat cct gaa	1122		
Val Asn Gln Asp Pro Asn Asn Asn Leu Gln Glu Gly Thr Asp Pro Glu			

330 335 340  
 act gaa gac ccc aac cac ctc cct cca gac agg gat gta cta gat ggc 1170  
 Thr Glu Asp Pro Asn His Leu Pro Pro Asp Arg Asp Val Leu Asp Gly

345 350 355  
 gag cag acc agc ccc tcc ttt atg agc aca gca tgg ctt gtc ttc aag 1218  
 Glu Gln Thr Ser Pro Ser Phe Met Ser Thr Ala Trp Leu Val Phe Lys

360 365 370 375  
 act ttc ttt gcc tct ctt ctt cca gaa ggc ccc cca gcc atc gca aac 1266  
 Thr Phe Phe Ala Ser Leu Leu Pro Glu Gly Pro Pro Ala Ile Ala Asn

380 385 390  
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 aacaaaaaat gcccaaggct tctcatgtgt ttattctgaa gagctttaat atatactcta 1506  
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 tgtataattg ctttttaaaa tgcagtgttt tacttttaac taaggggaac tttgcggagg 1806  
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<210> 32

<211> 391

<212> PRT

<213> Homo sapiens

<400> 32

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	20	25	30												
Ser	Val	Gly	His	Leu	Lys	Ala	His	Leu	Ser	Arg	Val	Tyr	Pro	Glu	Arg
	35	40	45												
Pro	Arg	Pro	Glu	Asp	Gln	Arg	Leu	Ile	Tyr	Ser	Gly	Lys	Leu	Leu	Leu
	50	55	60												
Asp	His	Gln	Cys	Leu	Arg	Asp	Leu	Leu	Pro	Lys	Gln	Glu	Lys	Arg	His
	65	70	75	80											
Val	Leu	His	Leu	Val	Cys	Asn	Val	Lys	Ser	Pro	Ser	Lys	Met	Pro	Glu
	85	90	95												
Ile	Asn	Ala	Lys	Val	Ala	Glu	Ser	Thr	Glu	Glu	Pro	Ala	Gly	Ser	Asn
	100	105	110												
Arg	Gly	Gln	Tyr	Pro	Glu	Asp	Ser	Ser	Ser	Asp	Gly	Leu	Arg	Gln	Arg
	115	120	125												
Glu	Val	Leu	Arg	Asn	Leu	Ser	Ser	Pro	Gly	Trp	Glu	Asn	Ile	Ser	Arg
	130	135	140												
Pro	Glu	Ala	Ala	Gln	Gln	Ala	Phe	Gln	Gly	Leu	Gly	Pro	Gly	Phe	Ser
	145	150	155	160											
Gly	Tyr	Thr	Pro	Tyr	Gly	Trp	Leu	Gln	Leu	Ser	Trp	Phe	Gln	Gln	Ile
	165	170	175												
Tyr	Ala	Arg	Gln	Tyr	Tyr	Met	Gln	Tyr	Leu	Ala	Ala	Thr	Ala	Ala	Ser
	180	185	190												
Gly	Ala	Phe	Val	Pro	Pro	Pro	Ser	Ala	Gln	Glu	Ile	Pro	Val	Val	Ser
	195	200	205												
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210	215	220	
Pro Ala Asn Gln Asn Ala Ala Pro Gln Val Val Val Asn Pro Gly Ala			
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Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Ile Val Glu Glu			
	245	250	255
Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala			
	260	265	270
Thr Phe Ser Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser			
	275	280	285
Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His			
	290	295	300
Val Gly Trp Phe Pro Phe Arg Pro Arg Pro Val Gln Asn Phe Pro Asn			
305	310	315	320
Asp Gly Pro Pro Pro Asp Val Val Asn Gln Asp Pro Asn Asn Asn Leu			
	325	330	335
Gln Glu Gly Thr Asp Pro Glu Thr Glu Asp Pro Asn His Leu Pro Pro			
	340	345	350
Asp Arg Asp Val Leu Asp Gly Glu Gln Thr Ser Pro Ser Phe Met Ser			
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Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu			
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Gly Pro Pro Ala Ile Ala Asn			
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<210> 33

<211> 4067

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (812).. (1138)

<400> 33

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Met Ser Ala Arg Gly Glu Gly

1

5

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Ala Gly Gln Pro Ser Thr Ser Ala Gln Gly Gln Pro Ala Ala Pro Ala

10

15

20

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cct cag aag aga gga cgc ggc cgc ccc agg aag cag cag caa gaa cca 928
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Pro Gln Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln Gln Gln Glu Pro

25

30

35

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 Lys Asn Lys Ser Pro Ser Lys Ala Ala Gln Lys Lys Ala Glu Ala Thr  
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 Gly Glu Lys Arg Pro Arg Gly Arg Pro Arg Lys Trp Pro Gln Gln Val  
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 Val Gln Lys Lys Pro Ala Gln Glu Glu Thr Glu Glu Thr Ser Ser Gln  
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<210> 34

<211> 109

<212> PRT

<213> Homo sapiens

<400> 34

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				20				25					30		
Arg	Lys	Gln	Gln	Gln	Glu	Pro	Thr	Gly	Glu	Pro	Ser	Pro	Lys	Arg	Pro
				35				40					45		
Arg	Gly	Arg	Pro	Lys	Gly	Ser	Lys	Asn	Lys	Ser	Pro	Ser	Lys	Ala	Ala
				50				55					60		
Gln	Lys	Lys	Ala	Glu	Ala	Thr	Gly	Glu	Lys	Arg	Pro	Arg	Gly	Arg	Pro
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Arg Lys Trp Pro Gln Gln Val Val Gln Lys Lys Pro Ala Gln Glu Glu

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90

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Thr Glu Glu Thr Ser Ser Gln Glu Ser Ala Glu Glu Asp

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105

<210> 35

<211> 4228

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148).. (1032)

<400> 35

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cccagctgcc caggaagagc cccagcc atg gaa cac cag ctc ctg tgc tgc gaa 174

Met Glu His Gln Leu Leu Cys Cys Glu

1

5

gtg gaa acc atc cgc cgc gcg tac ccc gat gcc aac ctc ctc aac gac 222

Val Glu Thr Ile Arg Arg Ala Tyr Pro Asp Ala Asn Leu Leu Asn Asp

10

15

20

25

cgg gtg ctg cgg gcc atg ctg aag gcg gag gag acc tgc gcg ccc tcg 270

Arg Val Leu Arg Ala Met Leu Lys Ala Glu Glu Thr Cys Ala Pro Ser

30

35

40

gtg tcc tac ttc aaa tgt gtg cag aag gag gtc ctg ccg tcc atg cgg 318

Val Ser Tyr Phe Lys Cys Val Gln Lys Glu Val Leu Pro Ser Met Arg

45

50

55

aag atc gtc gcc acc tgg atg ctg gag gtc tgc gag gaa cag aag tgc	366
Lys Ile Val Ala Thr Trp Met Leu Glu Val Cys Glu Glu Gln Lys Cys	
60 65 70	
gag gag gag gtc ttc ccg ctg gcc atg aac tac ctg gac cgc ttc ctg	414
Glu Glu Glu Val Phe Pro Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu	
75 80 85	
tcg ctg gag ccc gig aaa aag agc cgc ctg cag ctg ctg ggg gcc act	462
Ser Leu Glu Pro Val Lys Lys Ser Arg Leu Gln Leu Leu Gly Ala Thr	
90 95 100 105	
tgc atg ttc gtg gcc tct aag atg aag gag acc atc ccc ctg acg gcc	510
Cys Met Phe Val Ala Ser Lys Met Lys Glu Thr Ile Pro Leu Thr Ala	
110 115 120	
gag aag ctg tgc atc tac acc gac aac tcc atc cgg ccc gag gag ctg	558
Glu Lys Leu Cys Ile Tyr Thr Asp Asn Ser Ile Arg Pro Glu Glu Leu	
125 130 135	
ctg caa atg gag ctg ctc ctg gtg aac aag ctc aag tgg aac ctg gcc	606
Leu Gln Met Glu Leu Leu Leu Val Asn Lys Leu Lys Trp Asn Leu Ala	
140 145 150	
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Ala Met Thr Pro His Asp Phe Ile Glu His Phe Leu Ser Lys Met Pro	
155 160 165	
gag gcg gag gag aac aaa cag atc atc cgc aaa cac gcg cag acc ttc	702
Glu Ala Glu Glu Asn Lys Gln Ile Ile Arg Lys His Ala Gln Thr Phe	
170 175 180 185	
gtt gcc ctc tgt gcc aca gat gtg aag ttc att tcc aat ccg ccc tcc	750
Val Ala Leu Cys Ala Thr Asp Val Lys Phe Ile Ser Asn Pro Pro Ser	

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Met Val Ala Ala Gly Ser Val Val Ala Ala Val Gln Gly Leu Asn Leu			
205	210	215	
agg agc ccc aac aac ttc ctg tcc tac tac cgc ctc aca cgc ttc ctc			846
Arg Ser Pro Asn Asn Phe Leu Ser Tyr Tyr Arg Leu Thr Arg Phe Leu			
220	225	230	
tcc aga gtg atc aag tgt gac cca gac tgc ctc cgg gcc tgc cag gag			894
Ser Arg Val Ile Lys Cys Asp Pro Asp Cys Leu Arg Ala Cys Gln Glu			
235	240	245	
cag atc gaa gcc ctg ctg gag tca agc ctg cgc cag gcc cag cag aac			942
Gln Ile Glu Ala Leu Leu Glu Ser Ser Leu Arg Gln Ala Gln Gln Asn			
250	255	260	265
atg gac ccc aag gcc gcc gag gag gag gaa gag gag gag gag gag gtg			990
Met Asp Pro Lys Ala Ala Glu Glu Glu Glu Glu Glu Glu Glu Glu Val			
270	275	280	
gac ctg gct tgc aca ccc acc gac gtg cgg gac gtg gac atc			1032
Asp Leu Ala Cys Thr Pro Thr Asp Val Arg Asp Val Asp Ile			
285	290	295	
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<210> 36

<211> 295

<212> PRT

<213> Homo sapiens

<400> 36

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	35						40						45		
Gln	Lys	Glu	Val	Leu	Pro	Ser	Met	Arg	Lys	Ile	Val	Ala	Thr	Trp	Met
	50						55						60		
Leu	Glu	Val	Cys	Glu	Glu	Gln	Lys	Cys	Glu	Glu	Glu	Val	Phe	Pro	Leu
	65						70						75		80
Ala	Met	Asn	Tyr	Leu	Asp	Arg	Phe	Leu	Ser	Leu	Glu	Pro	Val	Lys	Lys
							85							90	95
Ser	Arg	Leu	Gln	Leu	Leu	Gly	Ala	Thr	Cys	Met	Phe	Val	Ala	Ser	Lys
	100									105				110	
Met	Lys	Glu	Thr	Ile	Pro	Leu	Thr	Ala	Glu	Lys	Leu	Cys	Ile	Tyr	Thr
	115									120				125	
Asp	Asn	Ser	Ile	Arg	Pro	Glu	Glu	Leu	Leu	Gln	Met	Glu	Leu	Leu	Leu
	130									135				140	
Val	Asn	Lys	Leu	Lys	Trp	Asn	Leu	Ala	Ala	Met	Thr	Pro	His	Asp	Phe
	145									150				155	160
Ile	Glu	His	Phe	Leu	Ser	Lys	Met	Pro	Glu	Ala	Glu	Glu	Asn	Lys	Gln
										165				170	175
Ile	Ile	Arg	Lys	His	Ala	Gln	Thr	Phe	Val	Ala	Leu	Cys	Ala	Thr	Asp
										180				185	190
Val	Lys	Phe	Ile	Ser	Asn	Pro	Pro	Ser	Met	Val	Ala	Ala	Gly	Ser	Val
	195									200				205	
Val	Ala	Ala	Val	Gln	Gly	Leu	Asn	Leu	Arg	Ser	Pro	Asn	Asn	Phe	Leu
	210									215				220	

Ser Tyr Tyr Arg Leu Thr Arg Phe Leu Ser Arg Val Ile Lys Cys Asp  
 225                      230                      235                      240  
 Pro Asp Cys Leu Arg Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Glu  
                          245                      250                      255  
 Ser Ser Leu Arg Gln Ala Gln Gln Asn Met Asp Pro Lys Ala Ala Glu  
                          260                      265                      270  
 Glu Glu Glu Glu Glu Glu Glu Glu Val Asp Leu Ala Cys Thr Pro Thr  
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 Asp Val Arg Asp Val Asp Ile  
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<210> 37

<211> 5007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (436).. (3402)

<400> 37

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 cgcccggcgc aggcacccgt gcctcccctc tgccaggaac ctiggggcct tglgtgtgac 180  
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 acctctgac aagtgcctag agggaigtgt gtgccagccc tcggtccagt gcccgtcct 300  
 gagctgactc ctgctggggc ccgacagctt gccgtgttcc ctgtgccigt agctccctgg 360  
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 cctcggcccc ggatc atg aaa ggc ctc ggt gac agc cgc ccc cgc cac ctc 471



Met Lys Gly Leu Gly Asp Ser Arg Pro Arg His Leu																
1				5				10								
tcc	gac	agc	cta	gac	cca	ccc	cac	gag	ccc	ctg	ttt	gca	ggg	acc	gac	519
Ser	Asp	Ser	Leu	Asp	Pro	Pro	His	Glu	Pro	Leu	Phe	Ala	Gly	Thr	Asp	
15				20				25								
cgc	aac	ccc	tac	ctg	ctg	tcg	ccc	acg	gag	gcc	ttc	gcc	cgc	gag	gcc	567
Arg	Asn	Pro	Tyr	Leu	Leu	Ser	Pro	Thr	Glu	Ala	Phe	Ala	Arg	Glu	Ala	
30				35				40								
cgc	ttc	ccc	ggg	cag	aac	acc	ctg	cca	gga	gat	ggc	ctc	ttt	ccc	ctc	615
Arg	Phe	Pro	Gly	Gln	Asn	Thr	Leu	Pro	Gly	Asp	Gly	Leu	Phe	Pro	Leu	
45				50				55				60				
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Asn	Asn	Gln	Leu	Pro	Pro	Pro	Ser	Ser	Thr	Phe	Pro	Arg	Ile	His	Tyr	
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aac	tcc	cac	ttc	gag	gtg	cca	gag	gag	agc	ccc	ttc	ccc	agc	cat	gcc	711
Asn	Ser	His	Phe	Glu	Val	Pro	Glu	Glu	Ser	Pro	Phe	Pro	Ser	His	Ala	
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caa	gcc	acc	aag	atc	aac	cgg	ctg	ccc	gcc	aac	ctc	ctg	gac	cag	ttt	759
Gln	Ala	Thr	Lys	Ile	Asn	Arg	Leu	Pro	Ala	Asn	Leu	Leu	Asp	Gln	Phe	
95				100				105								
gag	aag	cag	ctg	ccc	atc	cac	cgt	gat	ggc	ttc	agc	acc	ctc	caa	ttt	807
Glu	Lys	Gln	Leu	Pro	Ile	His	Arg	Asp	Gly	Phe	Ser	Thr	Leu	Gln	Phe	
110				115				120								
ccc	cgt	ggc	gag	gcc	aag	gcc	cgt	ggt	gag	agc	cct	ggc	cgc	atc	cgc	855
Pro	Arg	Gly	Glu	Ala	Lys	Ala	Arg	Gly	Glu	Ser	Pro	Gly	Arg	Ile	Arg	
125				130				135				140				

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His Leu Val His Ser Val Gln Arg Leu Phe Phe Thr Lys Ala Pro Ser	
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ctg gag ggc aca gcg ggc aag gtc ggt ggc aat ggc agc aag aag ggt	951
Leu Glu Gly Thr Ala Gly Lys Val Gly Gly Asn Gly Ser Lys Lys Gly	
160 165 170	
ggc atg gag gac ggc aag ggc cgg agg gcc aaa agc aag gag cgg gcc	999
Gly Met Glu Asp Gly Lys Gly Arg Arg Ala Lys Ser Lys Glu Arg Ala	
175 180 185	
aag gct ggg gag ccc aaa cgg cgc agc cgc tcc aac atc tca ggc tgg	1047
Lys Ala Gly Glu Pro Lys Arg Arg Ser Arg Ser Asn Ile Ser Gly Trp	
190 195 200	
tgg agc tcc gat gac aac ttg gac ggc gag gcc ggc gcc ttc cgc agc	1095
Trp Ser Ser Asp Asp Asn Leu Asp Gly Glu Ala Gly Ala Phe Arg Ser	
205 210 215 220	
agt ggc cca gcc tct ggg ctg atg ata cta ggc cgc cag gca gaa cgc	1143
Ser Gly Pro Ala Ser Gly Leu Met Ile Leu Gly Arg Gln Ala Glu Arg	
225 230 235	
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Ser Gln Pro Arg Tyr Phe Met His Ala Tyr Asn Thr Ile Ser Gly His	
240 245 250	
atg ctc aaa acc acc aag aac aac act act gag ctg act gcc cca cca	1239
Met Leu Lys Thr Thr Lys Asn Asn Thr Thr Glu Leu Thr Ala Pro Pro	
255 260 265	
ccc ccg ccc gca ccc cca gcc acc tgc ccc agc ctt ggg gtg ggc act	1287
Pro Pro Pro Ala Pro Pro Ala Thr Cys Pro Ser Leu Gly Val Gly Thr	
270 275 280	

gac acc aac tac gtc aaa cgg ggc tcc tgg tcc act ctg acc ctc agc 1335  
Asp Thr Asn Tyr Val Lys Arg Gly Ser Trp Ser Thr Leu Thr Leu Ser  
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His Ala His Glu Val Cys Gln Lys Thr Ser Ala Thr Leu Asp Lys Ser  
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ctg ctc aag tcc aaa tcc tgc cac cag ggt cta gcc tac cat tac ctg 1431  
Leu Leu Lys Ser Lys Ser Cys His Gln Gly Leu Ala Tyr His Tyr Leu  
320 325 330  
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Gln Val Pro Gly Gly Gly Gly Glu Trp Ser Thr Thr Leu Leu Ser Pro  
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Arg Glu Thr Asp Ala Ala Ala Glu Gly Pro Ile Pro Cys Arg Arg Met  
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Arg Ser Gly Ser Tyr Ile Lys Ala Met Gly Asp Glu Asp Ser Asp Glu  
365 370 375 380  
tcc ggc ggc agc ccc aag ccc tca ccc aag acc gcg gcg cgg cgc cag 1623  
Ser Gly Gly Ser Pro Lys Pro Ser Pro Lys Thr Ala Ala Arg Arg Gln  
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agc tat ctg agg gcc acg cag cag tcg ctg gga gag cag agc aac ccc 1671  
Ser Tyr Leu Arg Ala Thr Gln Gln Ser Leu Gly Glu Gln Ser Asn Pro  
400 405 410  
cgc agg agt ctg gac cgc ctg gat tca gtg gac atg ctg ctg ccc tcc 1719  
Arg Arg Ser Leu Asp Arg Leu Asp Ser Val Asp Met Leu Leu Pro Ser

415	420	425	
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Lys Cys Pro Ser Trp Glu Glu Asp Tyr Thr Pro Val Ser Asp Ser Leu			
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aac gac tcc agc tgc atc agc cag att ttt gga cag gcc tcc ctg atc			1815
Asn Asp Ser Ser Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile			
445	450	455	460
ccc cag ttg ttt ggc cat gag cag cag gta cgg gag gca gag ctg agt			1863
Pro Gln Leu Phe Gly His Glu Gln Gln Val Arg Glu Ala Glu Leu Ser			
465	470	475	
gac cag tat gag gcg gcc tgc gag tca gcc tgc agt gaa gcg gag tcc			1911
Asp Gln Tyr Glu Ala Ala Cys Glu Ser Ala Cys Ser Glu Ala Glu Ser			
480	485	490	
aca gcg gca gag acg ctt gac ttg cca ctg ccc agc tac ttc cgc tcc			1959
Thr Ala Ala Glu Thr Leu Asp Leu Pro Leu Pro Ser Tyr Phe Arg Ser			
495	500	505	
cgc agc cac agc tac ctg cgt gcc atc cag gca ggc tgc tgc cag gag			2007
Arg Ser His Ser Tyr Leu Arg Ala Ile Gln Ala Gly Cys Ser Gln Glu			
510	515	520	
gag gac agt gtc tcc ctg cag tcc ctc tcc cca ccg ccc agt acc ggc			2055
Glu Asp Ser Val Ser Leu Gln Ser Leu Ser Pro Pro Pro Ser Thr Gly			
525	530	535	540
agc ctc agc aat agt cgc acg ctt ccg agt tca tca tgc cta gtg gcg			2103
Ser Leu Ser Asn Ser Arg Thr Leu Pro Ser Ser Ser Cys Leu Val Ala			
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tat aag aag acc ccg cca ccg gtc cct cca cgc acc act tca aag ccg			2151
Tyr Lys Lys Thr Pro Pro Pro Val Pro Pro Arg Thr Thr Ser Lys Pro			

560	565	570	
ttc atc tca gtc aca gtc cag agc agt act gag tct gcc cag gac acc	2199		
Phe Ile Ser Val Thr Val Gln Ser Ser Thr Glu Ser Ala Gln Asp Thr			
575	580	585	
tac ctg gac agc cag gac cac aag agc gag gtg act agc cag tcg ggc	2247		
Tyr Leu Asp Ser Gln Asp His Lys Ser Glu Val Thr Ser Gln Ser Gly			
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ctg agc aac tcg tcg gac agc ctg gac agc agt acc cga ccg ccc agc	2295		
Leu Ser Asn Ser Ser Asp Ser Leu Asp Ser Ser Thr Arg Pro Pro Ser			
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gtg aca cgg ggt gga gtc gcc cca gcc cct gag gcc cca gag cca ccc	2343		
Val Thr Arg Gly Gly Val Ala Pro Ala Pro Glu Ala Pro Glu Pro Pro			
625	630	635	
cca aaa cat gca gct ctg aaa agt gaa caa ggg acg ctg acc agc tct	2391		
Pro Lys His Ala Ala Leu Lys Ser Glu Gln Gly Thr Leu Thr Ser Ser			
640	645	650	
gag tcc cac ccc gag gcc gcc ccc aaa agg aaa ctg tca tcg ata gga	2439		
Glu Ser His Pro Glu Ala Ala Pro Lys Arg Lys Leu Ser Ser Ile Gly			
655	660	665	
ata caa gag agg act aga agg aac ggt tcc cac ctc tcg gag gac aac	2487		
Ile Gln Glu Arg Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn			
670	675	680	
gga ccc aaa gcg atc gat gtg atg gca ccc tcc tca gaa agc agc gtc	2535		
Gly Pro Lys Ala Ile Asp Val Met Ala Pro Ser Ser Glu Ser Ser Val			
685	690	695	700
ccc tct cac agt atg tcc tcc cga cgg gac aca gac tcg gat acc cag	2583		

Pro Ser His Ser Met Ser Ser Arg Arg Asp Thr Asp Ser Asp Thr Gln	
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gat gcc aat gac tca agc tgt aag tca tct gag agg agc ctc ccg gac	2631
Asp Ala Asn Asp Ser Ser Cys Lys Ser Ser Glu Arg Ser Leu Pro Asp	
720 725 730	
tgt acc cct cac ccc aac tcc atc agc atc gat gcc ggt ccc cgg cag	2679
Cys Thr Pro His Pro Asn Ser Ile Ser Ile Asp Ala Gly Pro Arg Gln	
735 740 745	
gcc ccc aag att gcc cag atc aag cgc aac ctc tcc tat gga gac aac	2727
Ala Pro Lys Ile Ala Gln Ile Lys Arg Asn Leu Ser Tyr Gly Asp Asn	
750 755 760	
agc gac cct gcc cta gag gcg tcc tcg ctg ccc cca ccc gac ccc tgg	2775
Ser Asp Pro Ala Leu Glu Ala Ser Ser Leu Pro Pro Pro Asp Pro Trp	
765 770 775 780	
ctc gag acc tcc tcc agc tcc cca gca gag ccg gca cag cca ggg gcc	2823
Leu Glu Thr Ser Ser Ser Ser Pro Ala Glu Pro Ala Gln Pro Gly Ala	
785 790 795	
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Cys Arg Arg Asp Gly Tyr Trp Phe Leu Lys Leu Leu Gln Ala Glu Thr	
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gag cgg ctg gaa ggc tgg tgc tgc cag atg gac aag gag acc aaa gag	2919
Glu Arg Leu Glu Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu	
815 820 825	
aac aac ctc tct gaa gaa gtc tta gga aaa gtc ctc agt gct glg ggc	2967
Asn Asn Leu Ser Glu Glu Val Leu Gly Lys Val Leu Ser Ala Val Gly	
830 835 840	
agt gcc cag cta ctg atg tcc cag aaa ttc cag cag ttc cgg ggc ctc	3015

Ser	Ala	Gln	Leu	Leu	Met	Ser	Gln	Lys	Phe	Gln	Gln	Phe	Arg	Gly	Leu		
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tgt	gag	caa	aac	tig	aac	cct	gat	gcc	aac	cca	cgc	ccc	aca	gcc	cag	3063	
Cys	Glu	Gln	Asn	Leu	Asn	Pro	Asp	Ala	Asn	Pro	Arg	Pro	Thr	Ala	Gln		
			865						870					875			
gac	ctg	gca	ggg	ttc	tgg	gac	ctg	cta	cag	ctg	tcc	atc	gag	gat	atc	3111	
Asp	Leu	Ala	Gly	Phe	Trp	Asp	Leu	Leu	Gln	Leu	Ser	Ile	Glu	Asp	Ile		
		880						885				890					
agc	atg	aag	ttc	gat	gaa	ctc	tac	cac	ctc	aag	gcc	aac	agc	tgg	cag	3159	
Ser	Met	Lys	Phe	Asp	Glu	Leu	Tyr	His	Leu	Lys	Ala	Asn	Ser	Trp	Gln		
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ctg	gtg	gag	acc	ccc	gag	aag	agg	aag	gaa	gag	aag	aaa	cca	ccc	cct	3207	
Leu	Val	Glu	Thr	Pro	Glu	Lys	Arg	Lys	Glu	Glu	Lys	Lys	Pro	Pro	Pro		
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ccg	gtc	cca	aag	aag	cca	gcc	aaa	tcc	aag	ccg	gca	gtg	agc	cgc	gac	3255	
Pro	Val	Pro	Lys	Lys	Pro	Ala	Lys	Ser	Lys	Pro	Ala	Val	Ser	Arg	Asp		
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aag	gcc	tca	gac	gcc	agc	gac	aag	cag	cgc	cag	gag	gcc	cgc	aag	aga	3303	
Lys	Ala	Ser	Asp	Ala	Ser	Asp	Lys	Gln	Arg	Gln	Glu	Ala	Arg	Lys	Arg		
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ctc	ctg	gcg	gcc	aag	cgg	gca	gct	tct	gtg	cgg	cag	aac	tca	gcc	acc	3351	
Leu	Leu	Ala	Ala	Lys	Arg	Ala	Ala	Ser	Val	Arg	Gln	Asn	Ser	Ala	Thr		
			960						965				970				
gag	agc	gca	gac	agc	atc	gag	att	tat	gtc	ccg	gag	gcc	cag	acc	agg	3399	
Glu	Ser	Ala	Asp	Ser	Ile	Glu	Ile	Tyr	Val	Pro	Glu	Ala	Gln	Thr	Arg		
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ctc tgagaccatg caggaggaaa gaaacgatit taaatcatta aaaacacaaa 3452

Leu

aactaagtgc gaacggaaca gagttttctc aacctttgct atggttattc tgtctagaga 3512  
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ctcccagctt taggttatga agattttact cacaaaaaaaa atcaacaaaa atcacgaaac 3632  
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<210> 38

<211> 989

&lt;212&gt; PRT

<213> Homo sapiens

<400> 38

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Asp Pro Pro His Glu Pro Leu Phe Ala Gly Thr Asp Arg Asn Pro Tyr

20                      25                      30

Leu Leu Ser Pro Thr Glu Ala Phe Ala Arg Glu Ala Arg Phe Pro Gly

35                      40                      45

Gln Asn Thr Leu Pro Gly Asp Gly Leu Phe Pro Leu Asn Asn Gln Leu

50                      55                      60

Pro Pro Pro Ser Ser Thr Phe Pro Arg Ile His Tyr Asn Ser His Phe

65                      70                      75                      80

Glu Val Pro Glu Glu Ser Pro Phe Pro Ser His Ala Gln Ala Thr Lys

85                      90                      95

Ile Asn Arg Leu Pro Ala Asn Leu Leu Asp Gln Phe Glu Lys Gln Leu

100                      105                      110

Pro Ile His Arg Asp Gly Phe Ser Thr Leu Gln Phe Pro Arg Gly Glu

115                      120                      125

Ala Lys Ala Arg Gly Glu Ser Pro Gly Arg Ile Arg His Leu Val His

130                      135                      140

Ser Val Gln Arg Leu Phe Phe Thr Lys Ala Pro Ser Leu Glu Gly Thr

145                      150                      155                      160

Ala Gly Lys Val Gly Gly Asn Gly Ser Lys Lys Gly Gly Met Glu Asp			
	165	170	175
Gly Lys Gly Arg Arg Ala Lys Ser Lys Glu Arg Ala Lys Ala Gly Glu			
	180	185	190
Pro Lys Arg Arg Ser Arg Ser Asn Ile Ser Gly Trp Trp Ser Ser Asp			
	195	200	205
Asp Asn Leu Asp Gly Glu Ala Gly Ala Phe Arg Ser Ser Gly Pro Ala			
	210	215	220
Ser Gly Leu Met Ile Leu Gly Arg Gln Ala Glu Arg Ser Gln Pro Arg			
225	230	235	240
Tyr Phe Met His Ala Tyr Asn Thr Ile Ser Gly His Met Leu Lys Thr			
	245	250	255
Thr Lys Asn Asn Thr Thr Glu Leu Thr Ala Pro Pro Pro Pro Pro Ala			
	260	265	270
Pro Pro Ala Thr Cys Pro Ser Leu Gly Val Gly Thr Asp Thr Asn Tyr			
	275	280	285
Val Lys Arg Gly Ser Trp Ser Thr Leu Thr Leu Ser His Ala His Glu			
	290	295	300
Val Cys Gln Lys Thr Ser Ala Thr Leu Asp Lys Ser Leu Leu Lys Ser			
305	310	315	320
Lys Ser Cys His Gln Gly Leu Ala Tyr His Tyr Leu Gln Val Pro Gly			
	325	330	335
Gly Gly Gly Glu Trp Ser Thr Thr Leu Leu Ser Pro Arg Glu Thr Asp			
	340	345	350
Ala Ala Ala Glu Gly Pro Ile Pro Cys Arg Arg Met Arg Ser Gly Ser			
	355	360	365

Tyr Ile Lys Ala Met Gly Asp Glu Asp Ser Asp Glu Ser Gly Gly Ser  
370 375 380  
Pro Lys Pro Ser Pro Lys Thr Ala Ala Arg Arg Gln Ser Tyr Leu Arg  
385 390 395 400  
Ala Thr Gln Gln Ser Leu Gly Glu Gln Ser Asn Pro Arg Arg Ser Leu  
405 410 415  
Asp Arg Leu Asp Ser Val Asp Met Leu Leu Pro Ser Lys Cys Pro Ser  
420 425 430  
Trp Glu Glu Asp Tyr Thr Pro Val Ser Asp Ser Leu Asn Asp Ser Ser  
435 440 445  
Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile Pro Gln Leu Phe  
450 455 460  
Gly His Glu Gln Gln Val Arg Glu Ala Glu Leu Ser Asp Gln Tyr Glu  
465 470 475 480  
Ala Ala Cys Glu Ser Ala Cys Ser Glu Ala Glu Ser Thr Ala Ala Glu  
485 490 495  
Thr Leu Asp Leu Pro Leu Pro Ser Tyr Phe Arg Ser Arg Ser His Ser  
500 505 510  
Tyr Leu Arg Ala Ile Gln Ala Gly Cys Ser Gln Glu Glu Asp Ser Val  
515 520 525  
Ser Leu Gln Ser Leu Ser Pro Pro Pro Ser Thr Gly Ser Leu Ser Asn  
530 535 540  
Ser Arg Thr Leu Pro Ser Ser Ser Cys Leu Val Ala Tyr Lys Lys Thr  
545 550 555 560  
Pro Pro Pro Val Pro Pro Arg Thr Thr Ser Lys Pro Phe Ile Ser Val  
565 570 575  
Thr Val Gln Ser Ser Thr Glu Ser Ala Gln Asp Thr Tyr Leu Asp Ser

580	585	590
Gln Asp His Lys Ser Glu Val Thr Ser Gln Ser Gly Leu Ser Asn Ser		
595	600	605
Ser Asp Ser Leu Asp Ser Ser Thr Arg Pro Pro Ser Val Thr Arg Gly		
610	615	620
Gly Val Ala Pro Ala Pro Glu Ala Pro Glu Pro Pro Pro Lys His Ala		
625	630	635
Ala Leu Lys Ser Glu Gln Gly Thr Leu Thr Ser Ser Glu Ser His Pro		
645	650	655
Glu Ala Ala Pro Lys Arg Lys Leu Ser Ser Ile Gly Ile Gln Glu Arg		
660	665	670
Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn Gly Pro Lys Ala		
675	680	685
Ile Asp Val Met Ala Pro Ser Ser Glu Ser Ser Val Pro Ser His Ser		
690	695	700
Met Ser Ser Arg Arg Asp Thr Asp Ser Asp Thr Gln Asp Ala Asn Asp		
705	710	715
Ser Ser Cys Lys Ser Ser Glu Arg Ser Leu Pro Asp Cys Thr Pro His		
725	730	735
Pro Asn Ser Ile Ser Ile Asp Ala Gly Pro Arg Gln Ala Pro Lys Ile		
740	745	750
Ala Gln Ile Lys Arg Asn Leu Ser Tyr Gly Asp Asn Ser Asp Pro Ala		
755	760	765
Leu Glu Ala Ser Ser Leu Pro Pro Pro Asp Pro Trp Leu Glu Thr Ser		
770	775	780
Ser Ser Ser Pro Ala Glu Pro Ala Gln Pro Gly Ala Cys Arg Arg Asp		

785	790	795	800
Gly Tyr Trp Phe Leu Lys Leu Leu Gln Ala Glu Thr Glu Arg Leu Glu			
	805	810	815
Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu Asn Asn Leu Ser			
	820	825	830
Glu Glu Val Leu Gly Lys Val Leu Ser Ala Val Gly Ser Ala Gln Leu			
	835	840	845
Leu Met Ser Gln Lys Phe Gln Gln Phe Arg Gly Leu Cys Glu Gln Asn			
	850	855	860
Leu Asn Pro Asp Ala Asn Pro Arg Pro Thr Ala Gln Asp Leu Ala Gly			
865	870	875	880
Phe Trp Asp Leu Leu Gln Leu Ser Ile Glu Asp Ile Ser Met Lys Phe			
	885	890	895
Asp Glu Leu Tyr His Leu Lys Ala Asn Ser Trp Gln Leu Val Glu Thr			
	900	905	910
Pro Glu Lys Arg Lys Glu Glu Lys Lys Pro Pro Pro Pro Val Pro Lys			
	915	920	925
Lys Pro Ala Lys Ser Lys Pro Ala Val Ser Arg Asp Lys Ala Ser Asp			
	930	935	940
Ala Ser Asp Lys Gln Arg Gln Glu Ala Arg Lys Arg Leu Leu Ala Ala			
945	950	955	960
Lys Arg Ala Ala Ser Val Arg Gln Asn Ser Ala Thr Glu Ser Ala Asp			
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Ser Ile Glu Ile Tyr Val Pro Glu Ala Gln Thr Arg Leu			
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<210> 39

<211> 2522

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (1545)

<400> 39

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1 5 10 15

cgg ggc cag gtg gcc aag ctt gag gca gcc cta ggt gag gcc aag aag 96

Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu Gly Glu Ala Lys Lys

20 25 30

caa ctt cag gat gag atg ctg cgg cgg gtg gat gct gag aac agg ctg 144

Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu

35 40 45

cag acc atg aag gag gaa ctg gac ttc cag aag aac atc tac agt gag 192

Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu

50 55 60

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Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr Arg Leu Val Glu Ile

65 70 75 80

gac aat ggg aag cag cgt gag ttt gag agc cgg ctg gcg gat gcg ctg 288

Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg Leu Ala Asp Ala Leu

85 90 95

cag gaa ctg cgg gcc cag cat gag gac cag gtg gag cag tat aag aag 336

Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys

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Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser			
115	120	125	
gct gag agg aac agc aac ctg gtg ggg gct gcc cac gag gag ctg cag			432
Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln			
130	135	140	
cag tcg cgc atc cgc atc gac agc ctc tct gcc cag ctc agc cag ctc			480
Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu			
145	150	155	160
cag aag cag ctg gca gcc aag gag gcg aag ctt cga gac ctg gag gac			528
Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu Arg Asp Leu Glu Asp			
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tca ctg gcc cgt gag cgg gac acc agc cgg cgg ctg ctg gcg gaa aag			576
Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg Leu Leu Ala Glu Lys			
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Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala Leu Asp Met Glu Ile			
210	215	220	
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His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Arg Leu			
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Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr Lys Lys Arg Lys Leu	
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Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln His Ala Arg Thr Ser	
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ggg cgc gtg gcc gtg gag gag gtg gat gag gag ggc aag ttt gtc cgg	912
Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg	
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ctg cgc aac aag tcc aat gag gac cag tcc atg ggc aat tgg cag atc	960
Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met Gly Asn Trp Gln Ile	
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aag cgc cag aat gga gat gat ccc ttg ctg act tac cgg ttc cca cca	1008
Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr Tyr Arg Phe Pro Pro	
325	330
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Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr Ile Trp Ala Ala Gly	
340	345
gct ggg gcc acc cac agc ccc cct acc gac ctg gtg tgg aag gca cag	1104
Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu Val Trp Lys Ala Gln	
355	360
aac acc tgg ggc tgc ggg aac agc ctg cgt acg gct ctc atc aac tcc	1152
Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr Ala Leu Ile Asn Ser	
370	375
act ggg gaa gaa gtg gcc atg cgc aag ctg gtg cgc tca gtg act gtg	1200





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30

Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu

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Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg Leu Ala Asp Ala Leu		
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Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys		
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Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser		
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Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln		
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Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu		
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160		
Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu Arg Asp Leu Glu Asp		
165	170	175
Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg Leu Leu Ala Glu Lys		
180	185	190
Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met Gln Gln Gln Leu Asp		
195	200	205
Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala Leu Asp Met Glu Ile		
210	215	220
His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Arg Leu		
225	230	235
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Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly Arg Ala Ser Ser His		
245	250	255

Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr Lys Lys Arg Lys Leu			
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Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln His Ala Arg Thr Ser			
275	280	285	
Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg			
290	295	300	
Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met Gly Asn Trp Gln Ile			
305	310	315	320
Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr Tyr Arg Phe Pro Pro			
325	330	335	
Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr Ile Trp Ala Ala Gly			
340	345	350	
Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu Val Trp Lys Ala Gln			
355	360	365	
Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr Ala Leu Ile Asn Ser			
370	375	380	
Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val Arg Ser Val Thr Val			
385	390	395	400
Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp Leu Leu His His His			
405	410	415	
His Gly Ser His Cys Ser Ser Ser Gly Asp Pro Ala Glu Tyr Asn Leu			
420	425	430	
Arg Ser Arg Thr Val Leu Cys Gly Thr Cys Gly Gln Pro Ala Asp Lys			
435	440	445	
Ala Ser Ala Ser Gly Ser Gly Ala Gln Val Gly Gly Pro Ile Ser Ser			
450	455	460	

Gly Ser Ser Ala Ser Ser Val Thr Val Thr Arg Ser Tyr Arg Ser Val  
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 Gly Gly Ser Gly Gly Gly Ser Phe Gly Asp Asn Leu Val Thr Arg Ser  
                          485                      490                      495  
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                          Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr  
                          1                      5                      10  
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 Gln Tyr Gly Pro Ser Ser Ala Ala Met Ala Trp Arg Arg Gly Ser Met  
                          15                      20                      25  
 ggc gac tac atg gcc cag gag gac gac tgg gac cgg gac ctg ctg ctg 206  
 Gly Asp Tyr Met Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu  
                          30                      35                      40

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Asp Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser	
45 50 55	
aac tcc cac ctg cgg aag gca ggc aca cag atc gag aac att gat gag	302
Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu	
60 65 70 75	
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Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser	
80 85 90	
ggg gag cgg tta cct aag ccg gag cgg ggg aag atg aga gtg cac aaa	398
Gly Glu Arg Leu Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys	
95 100 105	
atc aac aat gtg aac aaa gcg ctg gac ttt att gcc agc aaa ggg atc	446
Ile Asn Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile	
110 115 120	
aag ctg gac ttc cat cgg gca gaa gag att gtg gac ggc aac gca aag	494
Lys Leu Asp Phe His Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys	
125 130 135	
atg acc ctg gga atg atc tgg acc atc atc ctt agg ttc gcc atc cag	542
Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln	
140 145 150 155	
gac atc tcc gtg gaa gag acc tcg gcc aag gaa ggg ctc ctt ctc tgg	590
Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp	
160 165 170	
tgc cag aga aag aca gcc cca tat aag aac gtc aat glg cag aac ttc	638
Cys Gln Arg Lys Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe	
175 180 185	

cac atc agc tgg aag gat ggt ctt gcc ttc aat gcc ctg atc cac cgg	686
His Ile Ser Trp Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg	
190 195 200	
cac aga cca gag ctg att gag tat gac aag ctg agg aag gac gac cct	734
His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro	
205 210 215	
gtc acc aac ctg aac aat gcc ttc gaa gtg gct gag aaa tac ctc gac	782
Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp	
220 225 230 235	
atc ccc aag atg ctg gat gca gag gac atc gtg aac acg gcc cgg ccc	830
Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro	
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gac gag aag gcc ata atg acc tat gtg tcc agc ttc tac cat gcc ttt	878
Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe	
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Ser Gly Ala Gln Lys Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys	
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Lys Val Leu Ala Val Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp	
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tac gag aag ctg gcc agc gac ctc ctg gag tgg atc cgg cgc acc atc	1022
Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile	
300 305 310 315	
ccc tgg ctg gag gac cgt gtg ccc caa aag act atc cag gag atg cag	1070
Pro Trp Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln	

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cag aag ctg gag gac ttc cgc gac tac cgg cgt gtg cac aag ccg ccc			1118
Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro			
335	340	345	
aag gtg cag gag aag tgc cag ctg gag atc aac ttc aac agc gtg cag			1166
Lys Val Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln			
350	355	360	
acc aag ctg cgc ctc agc aac cgg ccc gcc ttc atg ccc tcc gag ggc			1214
Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly			
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aag atg gtc tcg gac atc aac aat ggc tgg cag cac ttg gag cag gct			1262
Lys Met Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala			
380	385	390	395
gag aag ggc tac gag gag tgg ctg ctg aat gag att cgc agg ctg gag			1310
Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu			
400	405	410	
cgg ctc gac cac ctg gca gag aag ttc cgg cag aaa gcc tcc atc cac			1358
Arg Leu Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His			
415	420	425	
gag gcc tgg act gac ggg aag gaa gcc atg ctg aag cac cgg gac tac			1406
Glu Ala Trp Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr			
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gag acg gcc aca cta tcg gac atc aaa gcc ctc att cgc aag cac gag			1454
Glu Thr Ala Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu			
445	450	455	
gcc ttc gag agc gac ctg gct gcg cac cag gac cgc gtg gag cag atc			1502
Ala Phe Glu Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile			



460	465	470	475	
gcc gcc tcc gcc cag gag ctc aac gag ctg gat tac tac gac tcc cac	1550			
Ala Ala Ser Ala Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His				
480	485	490		
aat gtc aac acc cgg tgc cag aag atc tgt gac cag tgg gac gcc ctc	1598			
Asn Val Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu				
495	500	505		
ggc tct ctg aca cat agt cgc agg gaa gcc ctg gag aaa aca gag aag	1646			
Gly Ser Leu Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys				
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cag ctg gag gcc atc atc gac cag ctg cac ctg gaa tac gcc aag ccc	1694			
Gln Leu Glu Ala Ile Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro				
525	530	535		
gcg gcc ccc ttc aac aac tgg atg gag agc gcc atg gag gac ctc cag	1742			
Ala Ala Pro Phe Asn Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln				
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gac atg ttc atc gtc cat acc atc gag gag att gag ggc ctg atc tca	1790			
Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser				
560	565	570		
gcc cat gac cag ttc aag tcc acc ctg ccg gac gcc gat agg gag cgc	1838			
Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg				
575	580	585		
gag gcc atc ctg cat cca caa gga ggc cag agg atc gct gag agc aac	1886			
Glu Ala Ile Leu His Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn				
590	595	600		
cac atc aag ctg tcg ggc agc aac ccc tac acc acc gtc acc ccg caa	1934			

His	Ile	Lys	Leu	Ser	Gly	Ser	Asn	Pro	Tyr	Thr	Thr	Val	Thr	Pro	Gln		
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atc	atc	aac	tcc	aag	tgg	gag	aag	gtg	cag	cag	ctg	gtg	cca	aaa	cgg	1982	
Ile	Ile	Asn	Ser	Lys	Trp	Glu	Lys	Val	Gln	Gln	Leu	Val	Pro	Lys	Arg		
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cac	ctg	cgc	cgc	cag	ttc	gcc	agc	cag	gcc	aat	gtt	gtg	ggg	ccc	tgg	2078	
His	Leu	Arg	Arg	Gln	Phe	Ala	Ser	Gln	Ala	Asn	Val	Val	Gly	Pro	Trp		
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atc	cag	acc	aag	atg	gag	gag	atc	gcg	atc	tcc	att	gag	atg	aac	ggg	2126	
Ile	Gln	Thr	Lys	Met	Glu	Glu	Ile	Ala	Ile	Ser	Ile	Glu	Met	Asn	Gly		
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Thr	Leu	Glu	Asp	Gln	Leu	Ser	His	Leu	Lys	Gln	Tyr	Glu	Arg	Ser	Ile		
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gtg	gac	tac	aag	ccc	aac	ctg	gac	ctg	ctg	gag	cag	cag	cac	cag	ctc	2222	
Val	Asp	Tyr	Lys	Pro	Asn	Leu	Asp	Leu	Leu	Glu	Gln	Gln	His	Gln	Leu		
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Ile	Gln	Glu	Ala	Leu	Ile	Phe	Asp	Asn	Lys	His	Thr	Asn	Tyr	Thr	Met		
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gag	cac	atc	cgc	gtg	ggc	tgg	gag	cag	ctg	ctc	acc	acc	att	gcc	cgc	2318	
Glu	His	Ile	Arg	Val	Gly	Trp	Glu	Gln	Leu	Leu	Thr	Thr	Ile	Ala	Arg		
							735								740		
acc	atc	aac	gag	gtg	gag	aac	cag	atc	ctt	acc	cgc	gac	gcc	aag	ggc	2366	

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Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe	
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gac aag gat cat ggc ggg gcg ctg ggg cga gga gtt caa ggc ctg cct	2462
Asp Lys Asp His Gly Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro	
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cat cag cct ggg cta cga cgt gga gaa cga ccg gca ggt gag gcc gag	2510
His Gln Pro Gly Leu Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu	
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810	
ttc aac cgc atc atg agc ctg gtc gac ccc aac cat agc ggc ctt gtt	2558
Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val	
815	820
825	
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Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr	
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840	
gac acg gct gac cag gta atc act tcc ttc aag gtc cta gca ggg gac	2654
Asp Thr Ala Asp Gln Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp	
845	850
855	
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Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp	
860	865
870	875
cag gcc gag tac tgc atc gcc cgc atg gcg cca tac cag ggc cct gac	2750
Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp	
880	885
890	

ggc gtg cgc ggt gcc ctc gac tac aag tcc ttc tcc acg gcc ttg tat 2798

Gly Val Arg Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr

895

900

905

ggc gag agc gac ctg tgaggcccca gagacctgac ccaacacccc cgacgcctcc 2853

Gly Glu Ser Asp Leu

910

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 Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val Asn  
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 210 215 220  
 Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu  
 225 230 235 240  
 Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala Ile

245	250	255
Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys		
260	265	270
Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val		
275	280	285
Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp Tyr Glu Lys Leu Ala		
290	295	300
Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp		
305	310	315
Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp		
325	330	335
Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys		
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Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln Thr Lys Leu Arg Leu		
355	360	365
Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp		
370	375	380
Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu		
385	390	395
Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu		
405	410	415
Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp		
420	425	430
Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu		
435	440	445
Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp		

450	455	460	
Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ser Ala Gln			
465	470	475	480
Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg			
	485	490	495
Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His			
	500	505	510
Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile			
	515	520	525
Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro Ala Ala Pro Phe Asn			
	530	535	540
Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val			
545	550	555	560
His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe			
	565	570	575
Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu His			
	580	585	590
Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser			
	595	600	605
Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys			
	610	615	620
Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu			
625	630	635	640
Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu His Leu Arg Arg Gln			
	645	650	655
Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met			
	660	665	670

Glu	Glu	Ile	Ala	Ile	Ser	Ile	Glu	Met	Asn	Gly	Thr	Leu	Glu	Asp	Gln
675							680								685
Leu	Ser	His	Leu	Lys	Gln	Tyr	Glu	Arg	Ser	Ile	Val	Asp	Tyr	Lys	Pro
690							695								700
Asn	Leu	Asp	Leu	Leu	Glu	Gln	Gln	His	Gln	Leu	Ile	Gln	Glu	Ala	Leu
705						710						715			720
Ile	Phe	Asp	Asn	Lys	His	Thr	Asn	Tyr	Thr	Met	Glu	His	Ile	Arg	Val
						725						730			735
Gly	Trp	Glu	Gln	Leu	Leu	Thr	Thr	Ile	Ala	Arg	Thr	Ile	Asn	Glu	Val
						740						745			750
Glu	Asn	Gln	Ile	Leu	Thr	Arg	Asp	Ala	Lys	Gly	Ile	Ser	Gln	Glu	Gln
						755						760			765
Met	Gln	Glu	Phe	Arg	Ala	Ser	Phe	Asn	His	Phe	Asp	Lys	Asp	His	Gly
						770						775			780
Gly	Ala	Leu	Gly	Arg	Gly	Val	Gln	Gly	Leu	Pro	His	Gln	Pro	Gly	Leu
785						790						795			800
Arg	Arg	Gly	Glu	Arg	Pro	Ala	Gly	Glu	Ala	Glu	Phe	Asn	Arg	Ile	Met
						805						810			815
Ser	Leu	Val	Asp	Pro	Asn	His	Ser	Gly	Leu	Val	Thr	Phe	Gln	Ala	Phe
						820						825			830
Ile	Asp	Phe	Met	Ser	Arg	Glu	Thr	Thr	Asp	Thr	Asp	Thr	Ala	Asp	Gln
						835						840			845
Val	Ile	Thr	Ser	Phe	Lys	Val	Leu	Ala	Gly	Asp	Lys	Asn	Phe	Ile	Thr
						850						855			860
Ala	Glu	Glu	Leu	Arg	Arg	Glu	Leu	Pro	Pro	Asp	Gln	Ala	Glu	Tyr	Cys
865						870						875			880



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890

895

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905

910

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Met Pro Ser

1

acg gag aag gac ctg gcg gag gac gcg ccg tgg aag aag atc cag cag 166

Thr Glu Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln

5

10

15

aac aca ttc acg cgc tgg tgc aat gag cac ctc aag tgc gtg ggc aag 214

Asn Thr Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Gly Lys

20

25

30

35

cgc ctg acc gac ctg cag cgc gac ctc agc gac ggg ctc cgg ctc atc 262

Arg Leu Thr Asp Leu Gln Arg Asp Leu Ser Asp Gly Leu Arg Leu Ile

40

45

50

gcg ctg ctc gag gtc ctc agc cag aag cgc atg tac cgc aag ttc cat 310

Ala	Leu	Leu	Glu	Val	Leu	Ser	Gln	Lys	Arg	Met	Tyr	Arg	Lys	Phe	His	
			55					60					65			
ccg	cgc	ccc	aac	ttc	cgc	caa	atg	aag	ctg	gag	aac	gtg	tcc	gtg	gcc	358
Pro	Arg	Pro	Asn	Phe	Arg	Gln	Met	Lys	Leu	Glu	Asn	Val	Ser	Val	Ala	
			70					75					80			
ctc	gag	ttc	ctc	gag	cgc	gag	cac	atc	aag	ctc	gtg	tcc	ata	gac	agc	406
Leu	Glu	Phe	Leu	Glu	Arg	Glu	His	Ile	Lys	Leu	Val	Ser	Ile	Asp	Ser	
			85					90					95			
aag	gcc	atc	gtg	gat	ggg	aac	ctg	aag	ctg	atc	ctg	ggc	ctg	atc	tgg	454
Lys	Ala	Ile	Val	Asp	Gly	Asn	Leu	Lys	Leu	Ile	Leu	Gly	Leu	Ile	Trp	
100						105					110				115	
acg	ctg	atc	ctg	cac	tac	tcc	atc	tcc	atg	ccc	atg	tgg	gag	gat	gaa	502
Thr	Leu	Ile	Leu	His	Tyr	Ser	Ile	Ser	Met	Pro	Met	Trp	Glu	Asp	Glu	
						120					125				130	
gat	gat	gag	gat	gcc	cgc	aaa	cag	acg	ccc	aag	cag	cgg	ctg	ctt	ggc	550
Asp	Asp	Glu	Asp	Ala	Arg	Lys	Gln	Thr	Pro	Lys	Gln	Arg	Leu	Leu	Gly	
						135							140		145	
tgg	atc	cag	aac	aag	gtg	ccc	cag	ctg	ccc	atc	acc	aac	ttc	aac	cgt	598
Trp	Ile	Gln	Asn	Lys	Val	Pro	Gln	Leu	Pro	Ile	Thr	Asn	Phe	Asn	Arg	
						150							155		160	
gac	tgg	cag	gac	ggc	aaa	gct	ctg	ggc	gcc	ctg	gtg	gac	aac	tgc	gcc	646
Asp	Trp	Gln	Asp	Gly	Lys	Ala	Leu	Gly	Ala	Leu	Val	Asp	Asn	Cys	Ala	
						165							170		175	
ccc	ggt	ctc	tgc	ccc	gac	tgg	gag	gcc	tgg	gat	ccc	aac	cag	ccc	gtg	694
Pro	Gly	Leu	Cys	Pro	Asp	Trp	Glu	Ala	Trp	Asp	Pro	Asn	Gln	Pro	Val	
180								185					190		195	
gag	aac	tcc	cgg	gag	gcc	atg	cag	cag	gcc	gac	gac	tgg	ctt	ggg	gtg	742

Glu Asn Ser Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Val	
200	205
210	
ccc cag gtc att gcc cct gag gag att gtg gac ccc aac gtg gat gag	790
Pro Gln Val Ile Ala Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu	
215	220
225	
cat tct gtt atg acc tac ctg tcc cag ttc ccc aag gcc aag ctc aaa	838
His Ser Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys	
230	235
240	
cct ggt gcc cct gtt cga tcc aag cag ctg aac ccc aag aaa gcc atc	886
Pro Gly Ala Pro Val Arg Ser Lys Gln Leu Asn Pro Lys Lys Ala Ile	
245	250
255	
gcc tat ggg cct ggc atc gag cca cag ggc aac acc gtg ctg cag cct	934
Ala Tyr Gly Pro Gly Ile Glu Pro Gln Gly Asn Thr Val Leu Gln Pro	
260	265
270	275
gcc cac ttc acc gtg cag acg gtg gac gcg ggc gtg ggc gag gtg ctg	982
Ala His Phe Thr Val Gln Thr Val Asp Ala Gly Val Gly Glu Val Leu	
280	285
290	
gtc tac atc gag gac cct gaa ggc cac acc gag gag gct aag gtg gtt	1030
Val Tyr Ile Glu Asp Pro Glu Gly His Thr Glu Glu Ala Lys Val Val	
295	300
305	
ccc aac aat gac aag gat cgc acc tat gct gtc tcc tat gtg ccc aag	1078
Pro Asn Asn Asp Lys Asp Arg Thr Tyr Ala Val Ser Tyr Val Pro Lys	
310	315
320	
gtc gct ggg tta cac aag gtg acc gtg ctc ttt gct ggc cag aac att	1126
Val Ala Gly Leu His Lys Val Thr Val Leu Phe Ala Gly Gln Asn Ile	
325	330
335	

gaa cgc agt ccc ttt gag gtg aac gtg ggc atg gcc ctg gga gat gcc	1174		
Glu Arg Ser Pro Phe Glu Val Asn Val Gly Met Ala Leu Gly Asp Ala			
340	345	350	355
aac aag gtg tca gcc cgt ggc cct ggc ctg gaa cct gtg ggc aat gtg	1222		
Asn Lys Val Ser Ala Arg Gly Pro Gly Leu Glu Pro Val Gly Asn Val			
360	365	370	
gcc aac aaa ccc acc tac ttt gac atc tac act gcg ggg gcc ggc act	1270		
Ala Asn Lys Pro Thr Tyr Phe Asp Ile Tyr Thr Ala Gly Ala Gly Thr			
375	380	385	
ggc gat gtt gct gtg gtg atc gig gac cca cag ggc cgg cgg gac aca	1318		
Gly Asp Val Ala Val Val Ile Val Asp Pro Gln Gly Arg Arg Asp Thr			
390	395	400	
gtg gag gtg gcc ctg gag gac aag ggt gac agc acg ttc cgc tgc aca	1366		
Val Glu Val Ala Leu Glu Asp Lys Gly Asp Ser Thr Phe Arg Cys Thr			
405	410	415	
tac aga cct gcc atg gag ggg cca cat acc gtg cat gtg gcc ttt gcg	1414		
Tyr Arg Pro Ala Met Glu Gly Pro His Thr Val His Val Ala Phe Ala			
420	425	430	435
ggt gcc ccc atc acc cgc agt ccc ttc cct gtc cat gtg tgc gaa gcc	1462		
Gly Ala Pro Ile Thr Arg Ser Pro Phe Pro Val His Val Ser Glu Ala			
440	445	450	
tgt aac ccc aac gcc tgc cgc gcc tct ggg cga ggc ctg cag ccc aag	1510		
Cys Asn Pro Asn Ala Cys Arg Ala Ser Gly Arg Gly Leu Gln Pro Lys			
455	460	465	
ggt gtt cgc gtg aaa gag gtg gct gac ttc aag gtg ttt acc aag ggt	1558		
Gly Val Arg Val Lys Glu Val Ala Asp Phe Lys Val Phe Thr Lys Gly			
470	475	480	

gcc ggc agc ggg gag ctc aag gtc acg gtc aag ggg cca aag ggc aca	1606
Ala Gly Ser Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Thr	
485 490 495	
gag gag cca gtg aag gtg cgg gag gct ggg gat ggt gtg ttc gag tgc	1654
Glu Glu Pro Val Lys Val Arg Glu Ala Gly Asp Gly Val Phe Glu Cys	
500 505 510 515	
gag tac tac ccg gtg gtg cct ggg aag tat gtg gtg acc atc acg tgg	1702
Glu Tyr Tyr Pro Val Val Pro Gly Lys Tyr Val Val Thr Ile Thr Trp	
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ggc ggc tac gcc atc cct cgc agc ccc ttt gag gta cag gtg agc cca	1750
Gly Gly Tyr Ala Ile Pro Arg Ser Pro Phe Glu Val Gln Val Ser Pro	
535 540 545	
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Glu Ala Gly Val Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Thr	
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ggc cag gtg ggc aag tca gcc gat ttt gtg gtg gaa gcc att ggc acc	1846
Gly Gln Val Gly Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Thr	
565 570 575	
gag gtg ggg aca ctg ggc ttc tcc atc gag ggg ccc tca caa gcc aag	1894
Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser Gln Ala Lys	
580 585 590 595	
atc gaa tgt gac gat aag ggg gat ggc tcc tgc gat gtg cgg tac tgg	1942
Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp	
600 605 610	
ccc acg gag cct ggg gag tac gct gtg cac gtc atc tgt gac gat gag	1990
Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys Asp Asp Glu	

615	620	625	
gac atc cga gac tca ccc ttc att gcc cac atc ctg ccc gcc cca cct			2038
Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro Ala Pro Pro			
630	635	640	
gac tgc ttc cca gat aag gtg aag gcc ttt ggg cct ggc ctg gag cct			2086
Asp Cys Phe Pro Asp Lys Val Lys Ala Phe Gly Pro Gly Leu Glu Pro			
645	650	655	
acc ggc tgc atc gtg gac aag ccc gct gag ttc acc att gat gct cgt			2134
Thr Gly Cys Ile Val Asp Lys Pro Ala Glu Phe Thr Ile Asp Ala Arg			
660	665	670	675
gca gct ggc aag gga gac ctg aag ctc tat gcc cag gac gcc gac ggc			2182
Ala Ala Gly Lys Gly Asp Leu Lys Leu Tyr Ala Gln Asp Ala Asp Gly			
680	685	690	
tgt ccc atc gac atc aag gtg atc ccc aac ggc aac ggc acc ttc cgc			2230
Cys Pro Ile Asp Ile Lys Val Ile Pro Asn Gly Asn Gly Thr Phe Arg			
695	700	705	
tgc tcc tac gtg ccc acc aag ccc att aag cac acc atc atc atc tcc			2278
Cys Ser Tyr Val Pro Thr Lys Pro Ile Lys His Thr Ile Ile Ile Ser			
710	715	720	
tgg gga ggc gta aac gtg ccc aag agc ccc ttc cgg gtg aac gtg ggc			2326
Trp Gly Gly Val Asn Val Pro Lys Ser Pro Phe Arg Val Asn Val Gly			
725	730	735	
gag ggc agc cac ccc gag cgg gta aag gtg tac ggc ccc gga gtg gag			2374
Glu Gly Ser His Pro Glu Arg Val Lys Val Tyr Gly Pro Gly Val Glu			
740	745	750	755
aag aca ggc ctc aag gcc aat gag ccc acc tac ttc acg gtg gac tgc			2422
Lys Thr Gly Leu Lys Ala Asn Glu Pro Thr Tyr Phe Thr Val Asp Cys			

760	765	770	
agc gag gcg ggg caa ggc gac gtg agc atc ggc atc aag tgc gcc cca			2470
Ser Glu Ala Gly Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro			
775	780	785	
ggc gtg gtg ggc cct gca gag gct gac att gac ttc gac atc atc aag			2518
Gly Val Val Gly Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Ile Lys			
790	795	800	
aat gac aac gac acc ttc acc gtc aag tac acg cca cca ggg gcg ggc			2566
Asn Asp Asn Asp Thr Phe Thr Val Lys Tyr Thr Pro Pro Gly Ala Gly			
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Arg Tyr Thr Ile Met Val Leu Phe Ala Asn Gln Glu Ile Pro Ala Ser			
820	825	830	835
ccc ttc cac atc aag gtg gac cca tcc cac gat gcc agc aaa gtc aag			2662
Pro Phe His Ile Lys Val Asp Pro Ser His Asp Ala Ser Lys Val Lys			
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gcc gag ggc cct ggg ctg aat cgc aca ggt gtg gaa gtc ggg aag ccc			2710
Ala Glu Gly Pro Gly Leu Asn Arg Thr Gly Val Glu Val Gly Lys Pro			
855	860	865	
acc cac ttc acg gtg ctg acc aag gga gcc ggc aag gcc aag ctg gat			2758
Thr His Phe Thr Val Leu Thr Lys Gly Ala Gly Lys Ala Lys Leu Asp			
870	875	880	
gtg cag ttt gca ggg aca gcc aag ggc gag gtt gtg cgg gac ttt gag			2806
Val Gln Phe Ala Gly Thr Ala Lys Gly Glu Val Val Arg Asp Phe Glu			
885	890	895	
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Ile Ile Asp Asn His Asp Tyr Ser Tyr Thr Val Lys Tyr Thr Ala Val	
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Gln Gln Gly Asn Met Ala Val Thr Val Thr Tyr Gly Gly Asp Pro Val	
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Pro Lys Ser Pro Phe Val Val Asn Val Ala Pro Pro Leu Asp Leu Ser	
935 940 945	
aaa atc aaa gtt cag ggc ctt aat agc aag gtg gct gtg gga cag gaa	2998
Lys Ile Lys Val Gln Gly Leu Asn Ser Lys Val Ala Val Gly Gln Glu	
950 955 960	
caa gca ttc tct gtg aac aca cga ggg gct ggc ggt cag ggc caa ctg	3046
Gln Ala Phe Ser Val Asn Thr Arg Gly Ala Gly Gly Gln Gly Gln Leu	
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Asp Val Arg Met Thr Ser Pro Ser Arg Arg Pro Ile Pro Cys Lys Leu	
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Glu Pro Gly Gly Gly Ala Glu Ala Gln Ala Val Arg Tyr Met Pro Pro	
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Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr Glu Pro Gly	
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Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile Pro Gly Ser	
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ccc ttc aaa gcc acc att cgg cct gtg ttt gac ccg agc aag gtg cgg	3526
Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser Lys Val Arg	
1125	1130
1135	
gcc agt gga ccg ggc ctg gag cgc ggc aag gtc ggt gag gca gcc acc	3574
Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu Ala Ala Thr	
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1150	1155
ttc act gtg gac tgc tca gag gca ggc gag gcg gag ctg acc att gag	3622
Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu Thr Ile Glu	
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atc ctg tcg gat gcc ggg gtc aag gcc gag gtg ctg atc cac aac aac	3670
Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile His Asn Asn	
1175	1180
1185	

gcg gat ggc acc tac cac atc acc tac agc cct gcc ttc cct ggc acc	3718
Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe Pro Gly Thr	
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Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro Lys Phe Pro	
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acc cgt gtc cat gtg cag cct gcg gtc gat acc agt ggc gtc aag gtc	3814
Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly Val Lys Val	
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Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu Val Thr Thr	
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Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly Gly Asn His	
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Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr Asp Thr Tyr	
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Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr Thr Ala Tyr	
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Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu Val Ala Val	
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ccc aag agc ccc ttc cga gtg ggc gtg acc gag ggc tgt gat ccc acc	4102
Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys Asp Pro Thr	
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cgc gtc cga gcc ttc ggg cca ggc ctg gag ggt ggc ttg gtc aac aag	4150
Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu Val Asn Lys	
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gcc aac cga ttc act gtg gag acc agg gga gcg ggc acc ggg ggc ctt	4198
Ala Asn Arg Phe Thr Val Glu Thr Arg Gly Ala Gly Thr Gly Gly Leu	
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Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser Cys Lys Asp	
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Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe Thr Pro Gly	
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Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile Pro Gly Ser	
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Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg Val Pro Gln	
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Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro Leu Gln Val	
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Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu Val Arg Asp	

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Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala Thr Asp Gly				
	1480	1485	1490	
ccc tac acg gla gcc gtc aag tat gct gac cag gag gtg cca cgc agc				4630
Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val Pro Arg Ser				
	1495	1500	1505	
ccc ttc aag atc aag gtc ctc cca gct cat gat gcc agc aag gtg cgg				4678
Pro Phe Lys Ile Lys Val Leu Pro Ala His Asp Ala Ser Lys Val Arg				
	1510	1515	1520	
gcc agc ggg cca ggc ctc aac gcc tct ggc atc cct gcc agc ctg cct				4726
Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala Ser Leu Pro				
	1525	1530	1535	
gtg gag ttc acc atc gac gca cgg gac gcg ggc gag ggg ttg ctc act				4774
Val Glu Phe Thr Ile Asp Ala Arg Asp Ala Gly Glu Gly Leu Leu Thr				
1540	1545	1550	1555	
gtc cag atc ttg ggc ccc gag ggt aag ccc aag aag gcc aac atc cgg				4822
Val Gln Ile Leu Gly Pro Glu Gly Lys Pro Lys Lys Ala Asn Ile Arg				
	1560	1565	1570	
gac aat ggg gat ggc acg tac gct gtg tcc tac ctg ccg gac atg agt				4870
Asp Asn Gly Asp Gly Thr Tyr Ala Val Ser Tyr Leu Pro Asp Met Ser				
	1575	1580	1585	
ggc cgg tac acc atc acc atc aag tat ggc ggt gat gag atc ccc tac				4918
Gly Arg Tyr Thr Ile Thr Ile Lys Tyr Gly Gly Asp Glu Ile Pro Tyr				
	1590	1595	1600	
tcg ccc ttc cgc atc cat gct ctg ccc act ggg gat gcc agc aag tgc				4966
Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala Ser Lys Cys				

1605	1610	1615	
ctc gtc aca gtg tcc att gga ggc cat ggc ctg ggt gcc tgc ctg ggc	5014		
Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala Cys Leu Gly			
1620	1625	1630	1635
cct cga atc cag att ggg cag gag acg gtg atc acg gtg gat gcc aag	5062		
Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val Asp Ala Lys			
1640	1645	1650	
gca gcc ggt gag ggg aag gtg aca tgc acg gtg tcc acg ccg gat ggg	5110		
Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr Pro Asp Gly			
1655	1660	1665	
gca gag ctc gat gtg gat gtg gtt gag aac cat gac ggt acc ttt gac	5158		
Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly Thr Phe Asp			
1670	1675	1680	
atc tac tac aca gcg ccc gag ccg ggc aag tac gtc atc acc atc cgc	5206		
Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile Thr Ile Arg			
1685	1690	1695	
ttc ggg ggt gag cac atc ccc aac agc ccc ttc cac gtg ctg gcg tgt	5254		
Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val Leu Ala Cys			
1700	1705	1710	1715
gac ccc ctg ccg cac gag gag gag ccc tct gaa gtg cca cag ctg cgc	5302		
Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro Gln Leu Arg			
1720	1725	1730	
cag ccc tac gct cct ccc cgg ccc ggc gcc cgc ccc aca cac tgg gcc	5350		
Gln Pro Tyr Ala Pro Pro Arg Pro Gly Ala Arg Pro Thr His Trp Ala			
1735	1740	1745	
aca gag gag cca gtg gtg cct gtg gag cca atg gag tcc atg ctg agg	5398		

Thr Glu Glu Pro Val Val Pro Val Glu Pro Met Glu Ser Met Leu Arg	
1750	1755
1760	
ccc ttc aac ctg gtc atc ccc ttc gcg gtg cag aaa ggg gag ctc aca	5446
Pro Phe Asn Leu Val Ile Pro Phe Ala Val Gln Lys Gly Glu Leu Thr	
1765	1770
1775	
gga gag gtg cgg atg ccc tcg ggg aag acg gca cgg ccc aac atc acc	5494
Gly Glu Val Arg Met Pro Ser Gly Lys Thr Ala Arg Pro Asn Ile Thr	
1780	1785
1790	1795
gac aac aag gac ggc acc atc acg gtg agg tat gca ccc act gag aaa	5542
Asp Asn Lys Asp Gly Thr Ile Thr Val Arg Tyr Ala Pro Thr Glu Lys	
1800	1805
1810	
ggc ctg cac cag atg ggg atc aag tat gac ggc aac cac atc cct ggg	5590
Gly Leu His Gln Met Gly Ile Lys Tyr Asp Gly Asn His Ile Pro Gly	
1815	1820
1825	
agc ccc tta cag ttc tat gtg gat gcc atc aac agc cgc cat gtc agt	5638
Ser Pro Leu Gln Phe Tyr Val Asp Ala Ile Asn Ser Arg His Val Ser	
1830	1835
1840	
gcc tat ggg cca ggc ctg agc cat ggc atg gtc aac aag cca gcc acc	5686
Ala Tyr Gly Pro Gly Leu Ser His Gly Met Val Asn Lys Pro Ala Thr	
1845	1850
1855	
ttc act att gtc acc aaa gat gct gga gaa ggg ggt ctg tca ctg gcc	5734
Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala	
1860	1865
1870	1875
glg gag ggc cca tcc aag gca gag atc acc tgt aag gac aac aag gat	5782
Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp Asn Lys Asp	
1880	1885
1890	
ggc acc tgc acc gtg tcc tat ctg ccg act gcg cct gga gac tac agc	5830

Gly Thr Cys Thr Val Ser Tyr Leu Pro Thr Ala Pro Gly Asp Tyr Ser	
1895	1900
1905	
atc atc gtg cgc ttc gat gac aag cac atc ccg ggg agc ccc ttc aca	5878
Ile Ile Val Arg Phe Asp Asp Lys His Ile Pro Gly Ser Pro Phe Thr	
1910	1915
1920	
gcc aag atc aca ggt gat gac tcc atg agg acc tca cag ctg aat gtg	5926
Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln Leu Asn Val	
1925	1930
1935	
ggc acc tcc acg gac gtg tca ctg aag atc acc gag agt gat ctg agc	5974
Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser Asp Leu Ser	
1940	1945
1950	1955
cag ctg acc gcc agc atc cgt gcc ccc tcg ggc aac gag gag ccc tgc	6022
Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu Glu Pro Cys	
1960	1965
1970	
ctg ctg aag cgc ctg ccc aac cgg cac att ggg atc tcc ttc acc ccc	6070
Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser Phe Thr Pro	
1975	1980
1985	
aag gag gtc ggg gag cac gtg gtg agc gtg cgc aag agt ggc aag cat	6118
Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser Gly Lys His	
1990	1995
2000	
gtc acc aac agc ccc ttc aag atc ctg gtg ggg cca tct gag atc ggg	6166
Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser Glu Ile Gly	
2005	2010
2015	
gac gcc agc aag gtg cgg gtc tgg ggc aag ggg ctt tcc gag gga cac	6214
Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser Glu Gly His	
2020	2025
2030	2035

aca ttc cag gtg gca gag ttc atc gtg gac act cgc aat gca ggt tat	6262
Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn Ala Gly Tyr	
2040	2045
2050	
ggg ggc ttg ggg ctg agt att gaa ggc cca agc aag gtg gac atc aac	6310
Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn	
2055	2060
2065	
tgt gag gac atg gag gac ggg aca tgc aaa gtc acc tac tgc ccc acc	6358
Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr Cys Pro Thr	
2070	2075
2080	
gag ccc ggc acc tac atc atc aac atc aag ttt gct gac aag cac gtg	6406
Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp Lys His Val	
2085	2090
2095	
cct gga agc ccc ttc act gtg aag gtg acc ggc gag ggc cgc atg aag	6454
Pro Gly Ser Pro Phe Thr Val Lys Val Thr Gly Glu Gly Arg Met Lys	
2100	2105
2110	2115
gag agc atc acc cgg cgg aga cag gca cct tcc atc gcc acc atc ggc	6502
Glu Ser Ile Thr Arg Arg Arg Gln Ala Pro Ser Ile Ala Thr Ile Gly	
2120	2125
2130	
agc acc tgt gac ctc aac ctc aag atc cca gga aac tgg ttc cag atg	6550
Ser Thr Cys Asp Leu Asn Leu Lys Ile Pro Gly Asn Trp Phe Gln Met	
2135	2140
2145	
gtg tct gcc cag gag cgc ctg aca cgc acc ttc aca cgc agc agc cac	6598
Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg Ser Ser His	
2150	2155
2160	
acc tac acc cgc acg gag cgc acg gag atc agc aag acg cgg ggc ggg	6646
Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr Arg Gly Gly	
2165	2170
2175	



gag aca aag ccc gag gtg cgg gtg gag gag tcc acc cag gtc ggc ggg												6694
Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln Val Gly Gly												
2180			2185			2190			2195			
gac ccc ttc cct gct gtg ttt ggg gac ttc ctg ggc cgg gag cgc ctg												6742
Asp Pro Phe Pro Ala Val Phe Gly Asp Phe Leu Gly Arg Glu Arg Leu												
2200				2205				2210				
gga tcc ttc ggc agc atc acc cgg cag cag gag ggt gag gcc agc tct												6790
Gly Ser Phe Gly Ser Ile Thr Arg Gln Gln Glu Gly Glu Ala Ser Ser												
2215			2220			2225						
cag gac atg act gca cag gtg acc agc cca tcg ggc aag gtg gaa gcc												6838
Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys Val Glu Ala												
2230			2235			2240						
gca gag atc gtc gag ggc gag gac agc gcc tac agc gtc cgc ttt gtg												6886
Ala Glu Ile Val Glu Gly Glu Asp Ser Ala Tyr Ser Val Arg Phe Val												
2245			2250			2255						
ccc cag gaa atg ggg ccc cat acg gtc gct gtc aag tac cgt ggc cag												6934
Pro Gln Glu Met Gly Pro His Thr Val Ala Val Lys Tyr Arg Gly Gln												
2260			2265			2270			2275			
cac gtg ccc ggc agc ccc ttt cag ttc act gtg ggg ccg ctg ggt gaa												6982
His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu												
2280				2285				2290				
ggt ggt gcc cac aag gtg cgg gcc gga cga gca ggg ctg gag cga ggt												7030
Gly Gly Ala His Lys Val Arg Ala Gly Arg Ala Gly Leu Glu Arg Gly												
2295			2300			2305						
gtg gcc ggc glg cca gcc gag ttc agc atc tgg acc cgg gag gct ggc												7078
Val Ala Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly												

2310	2315	2320	
gct ggg ggc ctg tcc att gct gtg gag ggt cct agc aaa gcg gag att			7126
Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile			
2325	2330	2335	
gca ttt gag gat cgc aaa gat ggc tcc tgc ggc gtc tcc tat gtc gtc			7174
Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser Tyr Val Val			
2340	2345	2350	2355
cag gaa cca ggt gac tat gag gtc tcc atc aag ttc aat gat gag cac			7222
Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn Asp Glu His			
2360	2365	2370	
atc cca gac agc ccc ttt gtg gtg cct gtg gcc tcc ctc tcg gat gac			7270
Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu Ser Asp Asp			
2375	2380	2385	
gct cgc cgt ctc act gtc acc agc ctc cag gag acg ggg ctc aag gtg			7318
Ala Arg Arg Leu Thr Val Thr Ser Leu Gln Glu Thr Gly Leu Lys Val			
2390	2395	2400	
aac cag cca gcg tcc ttt gcc gtg cag ctg aac ggt gcc cgg ggc gtg			7366
Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala Arg Gly Val			
2405	2410	2415	
att gat gcc cgg gtg cac aca ccc tcg ggg gct gtg gag gag tgc tac			7414
Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu Glu Cys Tyr			
2420	2425	2430	2435
gtc tct gag ctg gac agt gac aag cac acc atc cgc ttc atc ccc cac			7462
Val Ser Glu Leu Asp Ser Asp Lys His Thr Ile Arg Phe Ile Pro His			
2440	2445	2450	
gag aat ggc gtc cac tcc atc gat gtc aag ttc aac ggt gcc cac atc			7510
Glu Asn Gly Val His Ser Ile Asp Val Lys Phe Asn Gly Ala His Ile			

2455	2460	2465	
cct gga agt ccc ttc aag atc cgc gtt ggg gag cag agc cag gct ggg			7558
Pro Gly Ser Pro Phe Lys Ile Arg Val Gly Glu Gln Ser Gln Ala Gly			
2470	2475	2480	
gac cca ggc ttg gtg tca gcc tac ggt cct ggg ctc gag gga ggc act			7606
Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu Gly Gly Thr			
2485	2490	2495	
acc ggt gtg tca tca gag ttc atc gtg aac acc ctg aat gcc ggc tcg			7654
Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn Ala Gly Ser			
2500	2505	2510	2515
ggg gcc ttg tct gtc acc att gat ggc ccc tcc aag gtg cag ctg gac			7702
Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val Gln Leu Asp			
2520	2525	2530	
tgt cgg gag tgt cct gag ggc cat gtg gtc act tat act ccc atg gcc			7750
Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr Pro Met Ala			
2535	2540	2545	
cct ggc aac tac ctc att gcc atc aag tac ggt ggc ccc cag cac atc			7798
Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro Gln His Ile			
2550	2555	2560	
gtg ggc agc ccc ttc aag gcc aag gtc act ggt ccg agg ctg tcc gga			7846
Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg Leu Ser Gly			
2565	2570	2575	
ggc cac agc ctt cac gaa aca tcc acg gtt ctg gtg gag act gtg acc			7894
Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu Thr Val Thr			
2580	2585	2590	2595
aag tcc tcc tca agc cgg ggc tcc agc tac agc tcc atc ccc aag ttc			7942

Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile Pro Lys Phe  
                   2600                          2605                          2610  
 tcc tca gat gcc agc aag gtg gtg act cgg ggc cct ggg ctg tcc cag 7990  
 Ser Ser Asp Ala Ser Lys Val Val Thr Arg Gly Pro Gly Leu Ser Gln  
                   2615                          2620                          2625  
 gcc ttc gtg ggc cag aag aac tcc ttc acc gtg gac tgc agc aaa gca 8038  
 Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys Ser Lys Ala  
                   2630                          2635                          2640  
 ggc acc aac atg atg atg gtg ggc gtg cac ggc ccc aag acc ccc tgt 8086  
 Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys Thr Pro Cys  
                   2645                          2650                          2655  
 gag gag gtg tac gtg aag cac atg ggg aac cgg gtg tac aat gtc acc 8134  
 Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr Asn Val Thr  
 2660                          2665                          2670                          2675  
 tac act gtc aag gag aaa ggg gac tac atc ctc att gtc aag tgg ggt 8182  
 Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val Lys Trp Gly  
                   2680                          2685                          2690  
 gac gaa agt gtc cct gga agc ccc ttc aaa gtc aag gtc cct 8224  
 Asp Glu Ser Val Pro Gly Ser Pro Phe Lys Val Lys Val Pro  
                   2695                          2700                          2705  
 tgaatcccaa aagtgcctcc ccagcctcag cccccacctc cagccacaca cacattacac 8284  
 acacacacac acacacacaa atgtgccaca cccagacacg cacagaatca gacactacaa 8344  
 acacctgcct tgggggigaa gtgaaggccc agcctcccca cccaccgcg cccaggggt 8404  
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 gggccaggct caggggcaga ggctgggaca caaggggctg gcgagggtg cgaggccagg 8524  
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gtcctggtctc tctggtggct acaaccccag agttttaagg acttggaag gaagcacaat 8704  
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 aactccaaat aaagtgcgcc tgcgcc 8971

<210> 44

<211> 2705

<212> PRT

<213> Homo sapiens

<400> 44

Met	Pro	Ser	Thr	Glu	Lys	Asp	Leu	Ala	Glu	Asp	Ala	Pro	Trp	Lys	Lys
1					5								10		15
Ile	Gln	Gln	Asn	Thr	Phe	Thr	Arg	Trp	Cys	Asn	Glu	His	Leu	Lys	Cys
			20					25					30		
Val	Gly	Lys	Arg	Leu	Thr	Asp	Leu	Gln	Arg	Asp	Leu	Ser	Asp	Gly	Leu
		35					40					45			
Arg	Leu	Ile	Ala	Leu	Leu	Glu	Val	Leu	Ser	Gln	Lys	Arg	Met	Tyr	Arg
	50					55					60				
Lys	Phe	His	Pro	Arg	Pro	Asn	Phe	Arg	Gln	Met	Lys	Leu	Glu	Asn	Val
65				70					75					80	
Ser	Val	Ala	Leu	Glu	Phe	Leu	Glu	Arg	Glu	His	Ile	Lys	Leu	Val	Ser
			85					90					95		
Ile	Asp	Ser	Lys	Ala	Ile	Val	Asp	Gly	Asn	Leu	Lys	Leu	Ile	Leu	Gly
			100					105					110		
Leu	Ile	Trp	Thr	Leu	Ile	Leu	His	Tyr	Ser	Ile	Ser	Met	Pro	Met	Trp

115	120	125	
Glu Asp Glu Asp Asp Glu Asp Ala Arg Lys Gln Thr Pro Lys Gln Arg			
130	135	140	
Leu Leu Gly Trp Ile Gln Asn Lys Val Pro Gln Leu Pro Ile Thr Asn			
145	150	155	160
Phe Asn Arg Asp Trp Gln Asp Gly Lys Ala Leu Gly Ala Leu Val Asp			
	165	170	175
Asn Cys Ala Pro Gly Leu Cys Pro Asp Trp Glu Ala Trp Asp Pro Asn			
	180	185	190
Gln Pro Val Glu Asn Ser Arg Glu Ala Met Gln Gln Ala Asp Asp Trp			
195	200	205	
Leu Gly Val Pro Gln Val Ile Ala Pro Glu Glu Ile Val Asp Pro Asn			
210	215	220	
Val Asp Glu His Ser Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala			
225	230	235	240
Lys Leu Lys Pro Gly Ala Pro Val Arg Ser Lys Gln Leu Asn Pro Lys			
	245	250	255
Lys Ala Ile Ala Tyr Gly Pro Gly Ile Glu Pro Gln Gly Asn Thr Val			
	260	265	270
Leu Gln Pro Ala His Phe Thr Val Gln Thr Val Asp Ala Gly Val Gly			
275	280	285	
Glu Val Leu Val Tyr Ile Glu Asp Pro Glu Gly His Thr Glu Glu Ala			
290	295	300	
Lys Val Val Pro Asn Asn Asp Lys Asp Arg Thr Tyr Ala Val Ser Tyr			
305	310	315	320
Val Pro Lys Val Ala Gly Leu His Lys Val Thr Val Leu Phe Ala Gly			

325	330	335
Gln Asn Ile Glu Arg Ser Pro Phe	Glu Val Asn Val Gly Met Ala Leu	
340	345	350
Gly Asp Ala Asn Lys Val Ser Ala Arg	Gly Pro Gly Leu Glu Pro Val	
355	360	365
Gly Asn Val Ala Asn Lys Pro Thr Tyr Phe	Asp Ile Tyr Thr Ala Gly	
370	375	380
Ala Gly Thr Gly Asp Val Ala Val Val Ile Val	Asp Pro Gln Gly Arg	
385	390	395
Arg Asp Thr Val Glu Val Ala Leu Glu Asp	Lys Gly Asp Ser Thr Phe	
405	410	415
Arg Cys Thr Tyr Arg Pro Ala Met Glu Gly	Pro His Thr Val His Val	
420	425	430
Ala Phe Ala Gly Ala Pro Ile Thr Arg Ser	Pro Phe Pro Val His Val	
435	440	445
Ser Glu Ala Cys Asn Pro Asn Ala Cys Arg	Ala Ser Gly Arg Gly Leu	
450	455	460
Gln Pro Lys Gly Val Arg Val Lys Glu Val	Ala Asp Phe Lys Val Phe	
465	470	475
Thr Lys Gly Ala Gly Ser Gly Glu Leu Lys	Val Thr Val Lys Gly Pro	
485	490	495
Lys Gly Thr Glu Glu Pro Val Lys Val Arg	Glu Ala Gly Asp Gly Val	
500	505	510
Phe Glu Cys Glu Tyr Tyr Pro Val Val Pro	Gly Lys Tyr Val Val Thr	
515	520	525
Ile Thr Trp Gly Gly Tyr Ala Ile Pro Arg	Ser Pro Phe Glu Val Gln	
530	535	540

Val Ser Pro Glu Ala Gly Val Gln Lys Val Arg Ala Trp Gly Pro Gly			
545	550	555	560
Leu Glu Thr Gly Gln Val Gly Lys Ser Ala Asp Phe Val Val Glu Ala			
	565	570	575
Ile Gly Thr Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser			
	580	585	590
Gln Ala Lys Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val			
	595	600	605
Arg Tyr Trp Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys			
	610	615	620
Asp Asp Glu Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro			
625	630	635	640
Ala Pro Pro Asp Cys Phe Pro Asp Lys Val Lys Ala Phe Gly Pro Gly			
	645	650	655
Leu Glu Pro Thr Gly Cys Ile Val Asp Lys Pro Ala Glu Phe Thr Ile			
	660	665	670
Asp Ala Arg Ala Ala Gly Lys Gly Asp Leu Lys Leu Tyr Ala Gln Asp			
	675	680	685
Ala Asp Gly Cys Pro Ile Asp Ile Lys Val Ile Pro Asn Gly Asn Gly			
	690	695	700
Thr Phe Arg Cys Ser Tyr Val Pro Thr Lys Pro Ile Lys His Thr Ile			
705	710	715	720
Ile Ile Ser Trp Gly Gly Val Asn Val Pro Lys Ser Pro Phe Arg Val			
	725	730	735
Asn Val Gly Glu Gly Ser His Pro Glu Arg Val Lys Val Tyr Gly Pro			
	740	745	750



Gly Val Glu Lys Thr Gly Leu Lys Ala Asn Glu Pro Thr Tyr Phe Thr			
755	760	765	
Val Asp Cys Ser Glu Ala Gly Gln Gly Asp Val Ser Ile Gly Ile Lys			
770	775	780	
Cys Ala Pro Gly Val Val Gly Pro Ala Glu Ala Asp Ile Asp Phe Asp			
785	790	795	800
Ile Ile Lys Asn Asp Asn Asp Thr Phe Thr Val Lys Tyr Thr Pro Pro			
805	810	815	
Gly Ala Gly Arg Tyr Thr Ile Met Val Leu Phe Ala Asn Gln Glu Ile			
820	825	830	
Pro Ala Ser Pro Phe His Ile Lys Val Asp Pro Ser His Asp Ala Ser			
835	840	845	
Lys Val Lys Ala Glu Gly Pro Gly Leu Asn Arg Thr Gly Val Glu Val			
850	855	860	
Gly Lys Pro Thr His Phe Thr Val Leu Thr Lys Gly Ala Gly Lys Ala			
865	870	875	880
Lys Leu Asp Val Gln Phe Ala Gly Thr Ala Lys Gly Glu Val Val Arg			
885	890	895	
Asp Phe Glu Ile Ile Asp Asn His Asp Tyr Ser Tyr Thr Val Lys Tyr			
900	905	910	
Thr Ala Val Gln Gln Gly Asn Met Ala Val Thr Val Thr Tyr Gly Gly			
915	920	925	
Asp Pro Val Pro Lys Ser Pro Phe Val Val Asn Val Ala Pro Pro Leu			
930	935	940	
Asp Leu Ser Lys Ile Lys Val Gln Gly Leu Asn Ser Lys Val Ala Val			
945	950	955	960
Gly Gln Glu Gln Ala Phe Ser Val Asn Thr Arg Gly Ala Gly Gly Gln			

965	970	975	
Gly Gln Leu Asp Val Arg Met Thr Ser Pro Ser Arg Arg Pro Ile Pro			
980	985	990	
Cys Lys Leu Glu Pro Gly Gly Gly Ala Glu Ala Gln Ala Val Arg Tyr			
995	1000	1005	
Met Pro Pro Glu Glu Gly Pro Tyr Lys Val Asp Ile Thr Tyr Asp Gly			
1010	1015	1020	
His Pro Val Pro Gly Ser Pro Phe Ala Val Glu Gly Val Leu Pro Pro			
1025	1030	1035	1040
Asp Pro Ser Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu			
1045	1050	1055	
Val Gly Thr Pro Ala Pro Phe Ser Ile Asp Thr Lys Gly Ala Gly Thr			
1060	1065	1070	
Gly Gly Leu Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Lys Ile Glu			
1075	1080	1085	
Cys Gln Asp Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr			
1090	1095	1100	
Glu Pro Gly Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile			
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Pro Gly Ser Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser			
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Lys Val Arg Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu			
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Ala Ala Thr Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu			
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Thr Ile Glu Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile			

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His Asn Asn Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe			
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Pro Gly Thr Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro			
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Lys Phe Pro Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly			
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Val Lys Val Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu			
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Val Thr Thr Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly			
	1250	1255	1260
Gly Asn His Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr			
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Asp Thr Tyr Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr			
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Thr Ala Tyr Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu			
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Val Ala Val Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys			
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Asp Pro Thr Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu			
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Val Asn Lys Ala Asn Arg Phe Thr Val Glu Thr Arg Gly Ala Gly Thr			
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Gly Gly Leu Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser			
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Cys Lys Asp Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe			
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Thr Pro Gly Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile			
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Pro Gly Ser Pro Phe Arg Val Pro Val Lys Asp Val Val Asp Pro Gly			
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Lys Val Lys Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg			
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Val Pro Gln Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro			
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Leu Gln Val Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu			
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Val Arg Asp Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala			
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Thr Asp Gly Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val			
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Lys Val Arg Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala			
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Ile Pro Tyr Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala			
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Ser Lys Cys Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala			
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Cys Leu Gly Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val			
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Asp Ala Lys Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr			
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Pro Asp Gly Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly			
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Thr Phe Asp Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile			
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Thr Ile Arg Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val			
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Leu Ala Cys Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro			
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Pro Ala Thr Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu			
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Ser Leu Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp			
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Pro Phe Thr Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln			
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Leu Asn Val Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser			
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Asp Leu Ser Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu			
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Glu Pro Cys Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser			
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Phe Thr Pro Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser			
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Gly Lys His Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser			
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Glu Ile Gly Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser			

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Ala Gly Tyr Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val			
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Asp Ile Asn Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr			
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Phe Gln Met Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg			
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Ser Ser His Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr			
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Arg Gly Gly Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln			
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2225	2230	2235	2240

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Glu Ala Gly Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys			
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Ala Glu Ile Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser			
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Tyr Val Val Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn			
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Asp Glu His Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu			
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Leu Lys Val Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala			
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Arg Gly Val Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu			
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Glu Cys Tyr Val Ser Glu Leu Asp Ser Asp Lys His Thr Ile Arg Phe			
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Gln Ala Gly Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu			
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Gly Gly Thr Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn			
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Ala Gly Ser Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val			
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Gln Leu Asp Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr			
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Pro Met Ala Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro			
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Gln His Ile Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg			
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Leu Ser Gly Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu			
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Thr Val Thr Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile			
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Pro Lys Phe Ser Ser Asp Ala Ser Lys Val Val Thr Arg Gly Pro Gly			
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Leu Ser Gln Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys			
2625	2630	2635	2640
Ser Lys Ala Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys			
	2645	2650	2655
Thr Pro Cys Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr			

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 gaccccgctg cgcacggcct glccgctgca caccagcttg ttggcgcttt cgtcgccgcg 180  
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Met Ser Ser Arg Ile Ala Arg Ala

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10 15 20

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 Thr Cys Pro Ala Ala Cys His Cys Pro Leu Glu Ala Pro Lys Cys Ala

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Ala Lys Gln Leu Asn Glu Asp Cys Ser Lys Thr Gln Pro Cys Asp His				
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acc aag ggg ctg gaa tgc aac ttc ggc gcc agc tcc acc gct ctg aag	473			
Thr Lys Gly Leu Glu Cys Asn Phe Gly Ala Ser Ser Thr Ala Leu Lys				
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ggg atc tgc aga gct cag tca gag ggc aga ccc tgt gaa tat aac tcc	521			
Gly Ile Cys Arg Ala Gln Ser Glu Gly Arg Pro Cys Glu Tyr Asn Ser				
90	95	100		
aga atc tac caa aac ggg gaa agt ttc cag ccc aac tgt aaa cat cag	569			
Arg Ile Tyr Gln Asn Gly Glu Ser Phe Gln Pro Asn Cys Lys His Gln				
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tgc aca tgt att gat ggc gcc gtg ggc tgc att cct ctg tgt ccc caa	617			
Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Ile Pro Leu Cys Pro Gln				
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Glu Leu Ser Leu Pro Asn Leu Gly Cys Pro Asn Pro Arg Leu Val Lys				
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gtt acc ggg cag tgc tgc gag gag tgg gtc tgt gac gag gat agt atc	713			
Val Thr Gly Gln Cys Cys Glu Glu Trp Val Cys Asp Glu Asp Ser Ile				
155	160	165		
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Phe Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn Glu Leu Ile Ala	
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Val Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val Phe Gly Met Glu	
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Pro Arg Ile Leu Tyr Asn Pro Leu Gln Gly Gln Lys Cys Ile Val Gln	
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Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr Gly Ile Ser	
235 240 245	
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Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys Glu Thr	
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Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Val Tyr Ser Ser Leu	
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Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys Lys Ser Pro Glu Pro Val	
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 His Lys Phe Arg Asp  
 380  
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Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp

35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys

50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe

65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu

85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser

100 105 110

Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val

115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly

130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu

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Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp

165 170 175

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Thr	Arg	Asn	Asn	Glu	Leu	Ile	Ala	Val	Gly	Lys	Gly	Ser	Ser	Leu	Lys
		195					200					205			
Arg	Leu	Pro	Val	Phe	Gly	Met	Glu	Pro	Arg	Ile	Leu	Tyr	Asn	Pro	Leu
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Glu	Cys	Arg	Leu	Val	Lys	Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys
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Gly	Gln	Pro	Val	Tyr	Ser	Ser	Leu	Lys	Lys	Gly	Lys	Lys	Cys	Ser	Lys
		275					280					285			
Thr	Lys	Lys	Ser	Pro	Glu	Pro	Val	Arg	Phe	Thr	Tyr	Ala	Gly	Cys	Leu
	290					295					300				
Ser	Val	Lys	Lys	Tyr	Arg	Pro	Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly
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Arg	Cys	Cys	Thr	Pro	Gln	Leu	Thr	Arg	Thr	Val	Lys	Met	Arg	Phe	Arg
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atg cca agc acc agc ttt cca gtc cct tcc aag ttt cca ctt ggc cct 287
Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro
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Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala
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Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr
            50            55            60
ctg ccg gcc ccg tgc cac aac ctt cag acc tcc aca ccg ggc atc atc 479
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile
            65            70            75            80

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Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala	
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Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu	
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Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val	
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Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro	
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Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser	
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Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro	
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Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly	

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Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His			
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aag acc acc ctg gag cag ccg ccc tca gtg gcg ctc aag gtg gag ccc	1295		
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Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro			

355	360	365	
gaa gac tac tcc tct ttc cag cac atc agg aag ggc ggc ttc tgc gac			1391
Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp			
370	375	380	
cag tac ctg gcg gtg ccg cag cac ccc tac cag tgg gcg aag ccc aag			1439
Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys			
385	390	395	400
ccc ctg tcc cct acg tcc tac atg agc ccg acc ctg ccc gcc ctg gac			1487
Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp			
405	410	415	
tgg cag ctg ccg tcc cac tca ggc ccg tat gag ctt cgg att gag gtg			1535
Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val			
420	425	430	
cag ccc aag tcc cac cac cga gcc cac tac gag acg gag ggc agc cgg			1583
Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg			
435	440	445	
ggg gcc gtg aag gcg tcg gcc gga gga cac ccc atc gtg cag ctg cat			1631
Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His			
450	455	460	
ggc tac tlg gag aat gag ccg ctg atg ctg cag ctt ttc att ggg acg			1679
Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr			
465	470	475	480
gcg gac gac cgc ctg ctg cgc ccg cac gcc ttc tac cag gtg cac cgc			1727
Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg			
485	490	495	
atc aca ggg aag acc gtg tcc acc acc agc cac gag gct atc ctc tcc			1775

Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser	
500	505
510	
aac acc aaa gtc ctg gag atc cca ctc ctg ccg gag aac agc atg cga	1823
Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg	
515	520
525	
gcc gtc att gac tgt gcc gga atc ctg aaa ctc aga aac tcc gac att	1871
Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile	
530	535
540	
gaa ctt cgg aaa gga gag acg gac atc ggg agg aag aac aca cgg gta	1919
Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val	
545	550
555	560
cgg ctg gtg ttc cgc gtt cac gtc ccg caa ccc agc ggc cgc acg ctg	1967
Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu	
565	570
575	
tcc ctg cag gtg gcc tcc aac ccc atc gaa tgc tcc cag cgc tca gct	2015
Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala	
580	585
590	
cag gag ctg cct ctg gtg gag aag cag agc acg gac agc tat ccg gtc	2063
Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val	
595	600
605	
gtg ggc ggg aag aag atg gtc ctg tct ggc cac aac ttc ctg cag gac	2111
Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp	
610	615
620	
tcc aag gtc att ttc gtg gag aaa gcc cca gat ggc cac cat gtc tgg	2159
Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp	
625	630
635	640
gag atg gaa gcg aaa act gac cgg gac ctg tgc aag ccg aat tct ctg	2207

Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu	
645	650
655	
gtg gtt gag atc ccg cca ttt cgg aat cag agg ata acc agc ccc gtt	2255
Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val	
660	665
670	
cac gtc agt ttc tac gtc tgc aac ggg aag aga aag cga agc cag tac	2303
His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr	
675	680
685	
cag cgt ttc acc tac ctt ccc gcc aac ggt aac gcc atc ttt cta acc	2351
Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr	
690	695
700	
gta agc cgt gaa cat gag cgc gtc ggg tgc ttt ttc taaagacgca	2397
Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe	
705	710
715	
gaaacgacgt cgccgtaaag cagcgtggcg tgttgcacat ttaactgtgt gatgtcccg	2457
tagtgagacc gagccatcga tgcctgaaa aggaaaggaa aagggaagct tcggatgcat	2517
tttccttgat ccctgttggg ggtggggggc ggggggttgc tactcagata gtcacggtta	2577
ttttgcttct tgcgaatgta taacagccaa ggggaaaaca tggctcttct gctccaaaaa	2637
actgaggggg tcctggtgtg catitgcacc ctaaagctgc ttacggtgaa aaggcaaata	2697
ggtatagcta ttttgcaggc accittagga ataaactttg ctitta	2743

<210> 48

<211> 716

<212> PRT

<213> Homo sapiens

<400> 48

Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro

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Ala Ala Ala Val Phe Gly Arg Gly Glu Thr Leu Gly Pro Ala Pro Arg			
20	25	30	
Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala			
35	40	45	
Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr			
50	55	60	
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile			
65	70	75	80
Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly			
85	90	95	
Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala			
100	105	110	
Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu			
115	120	125	
Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val			
130	135	140	
Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro			
145	150	155	160
Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser			
165	170	175	
Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn			
180	185	190	
Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro			
195	200	205	
Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly			

210	215	220	
Leu Gly Ala Cys Thr	Leu Leu Gly Ser Pro	Gln His Ser Pro	Ser Thr
225	230	235	240
Ser Pro Arg Ala Ser	Val Thr Glu Glu Ser	Trp Leu Gly Ala	Arg Ser
245	250	255	
Ser Arg Pro Ala Ser	Pro Cys Asn Lys	Arg Lys Tyr Ser	Leu Asn Gly
260	265	270	
Arg Gln Pro Pro Tyr	Ser Pro His His	Ser Pro Thr Pro	Ser Pro His
275	280	285	
Gly Ser Pro Arg Val	Ser Val Thr Asp	Asp Ser Trp Leu	Gly Asn Thr
290	295	300	
Thr Gln Tyr Thr Ser	Ser Ala Ile Val	Ala Ala Ile Asn	Ala Leu Thr
305	310	315	320
Thr Asp Ser Ser Leu	Asp Leu Gly Asp	Gly Val Pro Val	Lys Ser Arg
325	330	335	
Lys Thr Thr Leu Glu	Gln Pro Pro Ser	Val Ala Leu Lys	Val Glu Pro
340	345	350	
Val Gly Glu Asp Leu	Gly Ser Pro Pro	Pro Pro Ala Asp	Phe Ala Pro
355	360	365	
Glu Asp Tyr Ser Ser	Phe Gln His Ile	Arg Lys Gly Gly	Phe Cys Asp
370	375	380	
Gln Tyr Leu Ala Val	Pro Gln His Pro	Tyr Gln Trp Ala	Lys Pro Lys
385	390	395	400
Pro Leu Ser Pro Thr	Ser Tyr Met Ser	Pro Thr Leu Pro	Ala Leu Asp
405	410	415	
Trp Gln Leu Pro Ser	His Ser Gly Pro	Tyr Glu Leu Arg	Ile Glu Val
420	425	430	

Gln	Pro	Lys	Ser	His	His	Arg	Ala	His	Tyr	Glu	Thr	Glu	Gly	Ser	Arg
435							440						445		
Gly	Ala	Val	Lys	Ala	Ser	Ala	Gly	Gly	His	Pro	Ile	Val	Gln	Leu	His
450							455						460		
Gly	Tyr	Leu	Glu	Asn	Glu	Pro	Leu	Met	Leu	Gln	Leu	Phe	Ile	Gly	Thr
465							470						475		480
Ala	Asp	Asp	Arg	Leu	Leu	Arg	Pro	His	Ala	Phe	Tyr	Gln	Val	His	Arg
							485						490		495
Ile	Thr	Gly	Lys	Thr	Val	Ser	Thr	Thr	Ser	His	Glu	Ala	Ile	Leu	Ser
							500						505		510
Asn	Thr	Lys	Val	Leu	Glu	Ile	Pro	Leu	Leu	Pro	Glu	Asn	Ser	Met	Arg
							515						520		525
Ala	Val	Ile	Asp	Cys	Ala	Gly	Ile	Leu	Lys	Leu	Arg	Asn	Ser	Asp	Ile
							530						535		540
Glu	Leu	Arg	Lys	Gly	Glu	Thr	Asp	Ile	Gly	Arg	Lys	Asn	Thr	Arg	Val
545							550						555		560
Arg	Leu	Val	Phe	Arg	Val	His	Val	Pro	Gln	Pro	Ser	Gly	Arg	Thr	Leu
							565						570		575
Ser	Leu	Gln	Val	Ala	Ser	Asn	Pro	Ile	Glu	Cys	Ser	Gln	Arg	Ser	Ala
							580						585		590
Gln	Glu	Leu	Pro	Leu	Val	Glu	Lys	Gln	Ser	Thr	Asp	Ser	Tyr	Pro	Val
							595						600		605
Val	Gly	Gly	Lys	Lys	Met	Val	Leu	Ser	Gly	His	Asn	Phe	Leu	Gln	Asp
							610						615		620
Ser	Lys	Val	Ile	Phe	Val	Glu	Lys	Ala	Pro	Asp	Gly	His	His	Val	Trp
625							630						635		640



Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu

645

650

655

Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val

660

665

670

His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr

675

680

685

Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr

690

695

700

Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe

705

710

715

<210> 49

<211> 2353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (241).. (1482)

<400> 49

cgccgagacg agcagcggcc gagcagcgc gggcgcgggc gcaccgaggc gagggaggcg 60

gggaagcccc gccgccgccg ccccgcccgc ccttcccc gccgccgcc cctctcccc 120

ccgcccgtc gccgccttc tccctctgcc ttcttcccc acggccggcc gcctcctcgc 180

ccgcccgcc gcagccgagg agccgaggcc gccgcggccg tggcggcgga gccctcagcc 240

atg gcc tcg ggc gac acc ctc tac atc gcc acg gac ggc tcg gag atg 288

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met

1

5

10

15

ccg gcc gag atc gtg gag ctg cac gag atc gag gtg gag acc atc ccg 336



Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly	
165 170 175	
ggc aag aag agc ggc aag aag agt tac ctc agc ggc ggg gcc ggc gcg	816
Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala	
180 185 190	
gcg ggc ggg cgc ggc gcc gac ccg ggc aac aag aag tgg gag cag aag	864
Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys	
195 200 205	
cag gtg cag atc aag acc ctg gag ggc gag ttc tcg gtc acc atg tgg	912
Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp	
210 215 220	
tcc tca gat gaa aaa aaa gat att gac cat gag aca gtg gtt gaa gaa	960
Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu	
225 230 235 240	
cag atc att gga gag aac tca cct cct gat tat tca gaa tat atg aca	1008
Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr	
245 250 255	
gga aag aaa ctt cct cct gga gga ata cct ggc att gac ctc tca gat	1056
Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp	
260 265 270	
ccc aaa caa ctg gca gaa ttt gct aga atg aag cca aga aaa att aaa	1104
Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys	
275 280 285	
gaa gat gat gct cca aga aca ata gct tgc cct cat aaa ggc tgc aca	1152
Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr	
290 295 300	

aag atg ttc agg gat aac tcg gcc atg aga aaa cat ctg cac acc cac 1200  
Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His  
305 310 315 320  
ggt ccc aga gtc cac gtc tgt gca gaa tgt ggc aaa gct ttt gtt gag 1248  
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu  
325 330 335  
agt tca aaa cta aaa cga cac caa ctg gtt cat act gga gag aag ccc 1296  
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro  
340 345 350  
ttt cag tgc acg ttc gaa ggc tgt ggg aaa cgc ttt tca ctg gac ttc 1344  
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe  
355 360 365  
aat ttg cgc aca cat gtg cga atc cat acc gga gac agg ccc tat gtg 1392  
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val  
370 375 380  
tgc ccc ttc gat ggt tgt aat aag aag ttt gct cag tca act aac ctg 1440  
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu  
385 390 395 400  
aaa tct cac atc tta aca cat gct aag gcc aaa aac aac cag 1482  
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln  
405 410  
tgaaaagaag agagaagacc ctctcgcacc acgggaagca tcttccagaa gtgtgattgg 1542  
gaataaataat gcctctcctt tgtatattat ttctaggaag aattttaaaa atgaatccta 1602  
cacacctaag ggacatgttt tgataaagta gtaaaaatta aaaaaaaaaa actttactaa 1662  
gatgacattg ctaagaigct ctatcttgct ctgtaatctc gtttcaaaaa cacagtgttt 1722  
ttgtaaagtg tgggcccaac aggaggacaa ttcatgaact tcgcatcaaa agacaattct 1782  
ttatacaaca gtcctaaaaa tgggacttct ttccacattc ttataaataat gaagctcacc 1842

tgttgcttac aatTTTTTTa attttgtatt ttccaagtgt gcataatgta cactTTTTtg 1902  
 gggataigct tagtaatgct acgtgtgatt ttcttgagg ttgataactt tgcttgcagt 1962  
 agattttctt taaaagaatg ggcagttaca tgcatacttc aaaagtattt tcctgtaaaa 2022  
 aaaaaaaaaag ttatataggt ttgttttgct atcttaattt tggttgtatt ctttgaigtt 2082  
 aacacatttt gtataattgt atcgatagc tgtattgaat catgtagat caaatattag 2142  
 atgtgatita atagtgtaa tcaatttaa cccattttag tcactttttt ttccaaaaa 2202  
 aatactgcca gatgctgatg ttcagtgtaa ttctttgcc tgttcagta cagaaagtg 2262  
 tgctcagtiig tagaatgtat tgtacctttt aacacctgat ggtacatcc catgtaacag 2322  
 aaagggcaac aataaaatag caatcctaaa g 2353

<210> 50

<211> 414

<212> PRT

<213> Homo sapiens

<400> 50

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met

1 5 10 15

Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro

20 25 30

Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Asp

35 40 45

Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly

50 55 60

His Gly His Ala Gly His His His His His His His His His His

65 70 75 80

Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln

85 90 95

Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val			
100	105	110	
Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu			
115	120	125	
Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp			
130	135	140	
Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly			
145	150	155	160
Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly			
165	170	175	
Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala			
180	185	190	
Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys			
195	200	205	
Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp			
210	215	220	
Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu			
225	230	235	240
Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr			
245	250	255	
Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp			
260	265	270	
Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys			
275	280	285	
Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr			
290	295	300	

Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His  
 305                      310                      315                      320  
 Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu  
                          325                      330                      335  
 Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro  
                          340                      345                      350  
 Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe  
                          355                      360                      365  
 Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val  
                          370                      375                      380  
 Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu  
 385                      390                      395                      400  
 Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln  
                          405                      410

<210> 51

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222).. (950)

<400> 51

ataacgattt caagagctgc acttaagcat ctagaatttt ctgcgtcaca cctcttgaga 60  
 gaagagactg gctccaggtc tgactcagtc cactacaagc tagacggict tcttaaagca 120  
 ccaacattac ttgagicttt ggataaaatt gagaaaagag tctacaagta ttgtggactc 180  
 tacaggaggc aggaggctga caactggcag taaagacaaa g atg tca ggc ctg cgg 236

Met Ser Gly Leu Arg

1

5

ccc ggc act caa gtg gac cct gag att gag ctt ttt gta aag gct gga 284

Pro Gly Thr Gln Val Asp Pro Glu Ile Glu Leu Phe Val Lys Ala Gly

10

15

20

agt gat gga gag agt att gga aac tgt ccc ttt tgc caa cgc ctt ttc 332

Ser Asp Gly Glu Ser Ile Gly Asn Cys Pro Phe Cys Gln Arg Leu Phe

25

30

35

atg atc ctc tgg ctt aaa gga gtt aaa ttt aat gtg aca act gtt gac 380

Met Ile Leu Trp Leu Lys Gly Val Lys Phe Asn Val Thr Thr Val Asp

40

45

50

atg acc aga aag cct gaa gaa cta aag gac tta gcc cca ggt acc aat 428

Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu Ala Pro Gly Thr Asn

55

60

65

cct ccg ttc ctg gtg tat aac aag gag ttg aaa aca gac ttc att aaa 476

Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys Thr Asp Phe Ile Lys

70

75

80

85

att gag gag ttt tta gaa caa acc ctg gct cct cca agg tac cct cac 524

Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro Pro Arg Tyr Pro His

90

95

100

ctg agt ccc aag tac aag gag tct ttt gat gtg ggc tgt aac ctc ttt 572

Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val Gly Cys Asn Leu Phe

105

110

115

gcc aag ttt tct gca tac att aag aat aca caa aag gag gca aat aag 620

Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln Lys Glu Ala Asn Lys

120

125

130

aat ttt gaa aaa tct ctg ctc aaa gaa ttc aag cgt ctg gat gac tac 668



Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys Arg Leu Asp Asp Tyr  
 135 140 145  
 tta aac acc cca ctt ctg gat gaa att gat cca gac agt gct ggg gaa 716  
 Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro Asp Ser Ala Gly Glu  
 150 155 160 165  
 ccc cca gtt tcc aga aga cta ttc ttg gat ggg gac cag cta aca ctg 764  
 Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly Asp Gln Leu Thr Leu  
 170 175 180  
 gct gat tgt agc ttg tta ccc aag ctg aac att att aaa gtt gct gcc 812  
 Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile Ile Lys Val Ala Ala  
 185 190 195  
 aag aaa tat cgt gac ttt gac att cca gca gaa ttc tca gga gtc tgg 860  
 Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu Phe Ser Gly Val Trp  
 200 205 210  
 cgt tat ctc cac aat gcc tat gcc cgt gaa gaa ttt acc cac acg tgt 908  
 Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu Phe Thr His Thr Cys  
 215 220 225  
 cct gaa gac aaa gaa att gaa aat act tac gca aat gtg gct 950  
 Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala Asn Val Ala  
 230 235 240  
 taaacagaag agttaggaga gctcttacag gagaaaaggc tatatttgtg atcagatttt 1010  
 acttattgac atattagaaa ggtttttgca aataagaata tgaaaaatac tgtttcttct 1070  
 atccaactct cttatgaaaa ggaactctgt attttctatt agccataaat aatctgtcca 1130  
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 gcaatcciga atgacatgga aagcatcaca aaaaaaaaaa 1229

<210> 52

<211> 243

<212> PRT

<213> Homo sapiens

<400> 52

Met	Ser	Gly	Leu	Arg	Pro	Gly	Thr	Gln	Val	Asp	Pro	Glu	Ile	Glu	Leu
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Phe	Val	Lys	Ala	Gly	Ser	Asp	Gly	Glu	Ser	Ile	Gly	Asn	Cys	Pro	Phe
				20				25					30		
Cys	Gln	Arg	Leu	Phe	Met	Ile	Leu	Trp	Leu	Lys	Gly	Val	Lys	Phe	Asn
				35				40					45		
Val	Thr	Thr	Val	Asp	Met	Thr	Arg	Lys	Pro	Glu	Glu	Leu	Lys	Asp	Leu
				50				55					60		
Ala	Pro	Gly	Thr	Asn	Pro	Pro	Phe	Leu	Val	Tyr	Asn	Lys	Glu	Leu	Lys
				65				70					75		80
Thr	Asp	Phe	Ile	Lys	Ile	Glu	Glu	Phe	Leu	Glu	Gln	Thr	Leu	Ala	Pro
								85					90		95
Pro	Arg	Tyr	Pro	His	Leu	Ser	Pro	Lys	Tyr	Lys	Glu	Ser	Phe	Asp	Val
								100					105		110
Gly	Cys	Asn	Leu	Phe	Ala	Lys	Phe	Ser	Ala	Tyr	Ile	Lys	Asn	Thr	Gln
								115					120		125
Lys	Glu	Ala	Asn	Lys	Asn	Phe	Glu	Lys	Ser	Leu	Leu	Lys	Glu	Phe	Lys
								130					135		140
Arg	Leu	Asp	Asp	Tyr	Leu	Asn	Thr	Pro	Leu	Leu	Asp	Glu	Ile	Asp	Pro
								145					150		155
Asp	Ser	Ala	Gly	Glu	Pro	Pro	Val	Ser	Arg	Arg	Leu	Phe	Leu	Asp	Gly
													165		170
															175

Asp Gln Leu Thr Leu Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile  
                   180                  185                  190  
 Ile Lys Val Ala Ala Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu  
                   195                  200                  205  
 Phe Ser Gly Val Trp Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu  
                   210                  215                  220  
 Phe Thr His Thr Cys Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala  
 225                  230                  235                  240  
 Asn Val Ala

<210> 53

<211> 4001

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (316)

<400> 53

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Pro Gly Asn Pro Tyr Val Lys Val Asn Val Tyr Tyr Gly Arg Lys Arg

1                  5                  10                  15

att gcc aag aag aaa acc cat gtg aag aag tgc act ttg aac ccc atc 97

Ile Ala Lys Lys Lys Thr His Val Lys Lys Cys Thr Leu Asn Pro Ile

20                  25                  30

ttc aat gaa tct ttc atc tac gac atc ccc act gac ctc ctg cct gat 145

Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp

35                  40                  45

atc agc atc gag ttc ctc gtt atc gac ttc gat cgc acc acc aag aat 193  
 Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn  
 50 55 60  
 gag gtg gtg ggg agg ctg atc ctg ggg gca cac agt gtc aca gcc agt 241  
 Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser  
 65 70 75 80  
 ggt gct gaa cac tgg aga gag gtc tgc gag agc ccc cgc aag cct gtg 289  
 Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val  
 85 90 95  
 gcc aag tgg cac agt ctg agc gag tac taatcctgtt cttctctcct 336  
 Ala Lys Trp His Ser Leu Ser Glu Tyr  
 100 105  
 ctaatccccg ggggccaagc tggggaggga tgtggagggg aaaaagatga cagagaagtg 396  
 gactccaaac ctcatcttag ttgtagaaga aaatttctta caaaacaaat tccacaaaga 456  
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 acatt 4001

<210> 54

<211> 105

<212> PRT

<213> Homo sapiens

<400> 54



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Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser				
20	25	30		
gca gaa agc cag att ctt aag cac ctt ctg aaa aat ctt ttc aag ata	261			
Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile				
35	40	45		
ttc tgc cta gac ggt gtg aag gga gac ctg ctg att gac atc ggc tct	309			
Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser				
50	55	60		
ggc ccc act atc tat cag ctc ctc tct gct tgt gaa tcc ttt aag gag	357			
Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu				
65	70	75	80	
atc gtc gtc act gac tac tca gac cag aac ctg cag gag ctg gag aag	405			
Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys				
85	90	95		
tgg ctg aag aaa gag cca gag gcc ttt gac tgg tcc cca gtg gtg acc	453			
Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr				
100	105	110		
tat gtg tgt gat ctt gaa ggg aac aga gtc aag ggt cca gag aag gag	501			
Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu				
115	120	125		
gag aag ttg aga cag gcg gtc aag cag gtg ctg aag tgt gat gtg act	549			
Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr				
130	135	140		
cag agc cag cca ctg ggg gcc gtc ccc tta ccc ccg gct gac tgc gtg	597			
Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val				



145	150	155	160	
ctc agc aca ctg tgt ctg gat gcc gcc tgc cca gac ctc ccc acc tac	645			
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr				
165	170	175		
tgc agg gcg ctc agg aac ctc ggc agc cta ctg aag cca ggg ggc ttc	693			
Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe				
180	185	190		
ctg gtg atc atg gat gcg ctc aag agc agc tac tac atg att ggt gag	741			
Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu				
195	200	205		
cag aag ttc tcc agc ctc ccc ctg ggc cgg gag gca gta gag gct gct	789			
Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala				
210	215	220		
gtg aaa gag gct ggc tac aca atc gaa tgg ttt gag gtg atc tcg caa	837			
Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln				
225	230	235	240	
agt tat tct tcc acc atg gcc aac aac gaa gga ctt ttc tcc ctg gtg	885			
Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val				
245	250	255		
gcg agg aag ctg agc aga ccc ctg tga tgcctgt gacctcaatt aaagcaattc	939			
Ala Arg Lys Leu Ser Arg Pro Leu				
260				
ctttgacctg tca	952			

<210> 56

<211> 264

<212> PRT

<213> Homo sapiens

<400> 56

Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His Phe Asn

1 5 10 15

Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser

20 25 30

Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile

35 40 45

Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser

50 55 60

Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu

65 70 75 80

Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys

85 90 95

Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr

100 105 110

Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu

115 120 125

Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr

130 135 140

Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val

145 150 155 160

Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr

165 170 175

Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe

180 185 190

Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu  
 195 200 205  
 Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala  
 210 215 220  
 Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln  
 225 230 235 240  
 Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val  
 245 250 255  
 Ala Arg Lys Leu Ser Arg Pro Leu  
 260

<210> 57

<211> 2617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94).. (633)

<400> 57

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Met Ala Pro Gly Val Ala Arg

1

5

ggg ccg acg ccg tac tgg agg ttg cgc ctc ggt ggc gcc gcg ctg ctc 162

Gly Pro Thr Pro Tyr Trp Arg Leu Arg Leu Gly Gly Ala Ala Leu Leu

10

15

20

ctg ctg ctc atc ccg gtg gcc gcc gcg cag gag cct ccc gga gct gct 210

Leu Leu Leu Ile Pro Val Ala Ala Ala Gln Glu Pro Pro Gly Ala Ala	
25 30 35	
tgt tct cag aac aca aac aaa acc tgt gaa gag tgc ctg aag aac gtc	258
Cys Ser Gln Asn Thr Asn Lys Thr Cys Glu Glu Cys Leu Lys Asn Val	
40 45 50 55	
tcc tgt ctt tgg tgc aac act aac aag gct tgt ctg gac tac cca gtt	306
Ser Cys Leu Trp Cys Asn Thr Asn Lys Ala Cys Leu Asp Tyr Pro Val	
60 65 70	
aca agc gtc ttg cca ccg gct tcc ctt tgt aaa ttg agc tct gca cgc	354
Thr Ser Val Leu Pro Pro Ala Ser Leu Cys Lys Leu Ser Ser Ala Arg	
75 80 85	
tgg gga gtt tgt tgg gtg aac ttt gag gcg ctg atc atc acc atg tgc	402
Trp Gly Val Cys Trp Val Asn Phe Glu Ala Leu Ile Ile Thr Met Ser	
90 95 100	
gta gtc ggg gga acc ctc ctc ctg ggc att gcc atc tgc tgc tgc tgc	450
Val Val Gly Gly Thr Leu Leu Leu Gly Ile Ala Ile Cys Cys Cys Cys	
105 110 115	
tgc tgc agg agg aag agg agc cgg aag ccg gac agg agt gag gag aag	498
Cys Cys Arg Arg Lys Arg Ser Arg Lys Pro Asp Arg Ser Glu Glu Lys	
120 125 130 135	
gcc atg cgt gag cgg gag gag agg cgg ata cgg cag gag gaa cgg aga	546
Ala Met Arg Glu Arg Glu Glu Arg Arg Ile Arg Gln Glu Glu Arg Arg	
140 145 150	
gca gag atg aag aca aga cat gat gaa atc aga aaa aaa tat ggc ctg	594
Ala Glu Met Lys Thr Arg His Asp Glu Ile Arg Lys Lys Tyr Gly Leu	
155 160 165	
ttt aaa gaa gaa aac ccg tat gct aga ttt gaa aac aac taaagcgctc	643

Phe Lys Glu Glu Asn Pro Tyr Ala Arg Phe Glu Asn Asn

170

175

180

cagcacatca gtcceagcgc ticcigigag gtgcactccg cagcccagcc cagccgggag 703  
accacgtggc cattgceggc tccigaccit ggccagtga cctgccagcc ticcaggaca 763  
ggcggccgga gagctgcccc tgaaggacag tcctctcgtc ttgcagactg gtgaccttct 823  
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cagttcttca ggctgatttc cctgacctct tgggcatttg tatttgtagt aaagtattgc 2263  
agagattcct aagtatttta tagcagccat caaaattgga ctttgtattg tttattcata 2323  
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tagtcagccc ttgcgctcag tgtagaaacc cacgtctgta aggtcggict tcttccatct 2503  
gcttttttct gaaatacact aagagcagcc aaaaaactgt aaccicaagg aaaccataaa 2563  
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<210> 58

<211> 180

<212> PRT

<213> Homo sapiens

<400> 58

Met Ala Pro Gly Val Ala Arg Gly Pro Thr Pro Tyr Trp Arg Leu Arg

1 5 10 15

Leu Gly Gly Ala Ala Leu Leu Leu Leu Leu Ile Pro Val Ala Ala Ala

20 25 30

Gln Glu Pro Pro Gly Ala Ala Cys Ser Gln Asn Thr Asn Lys Thr Cys

35 40 45

Glu Glu Cys Leu Lys Asn Val Ser Cys Leu Trp Cys Asn Thr Asn Lys

50 55 60

Ala Cys Leu Asp Tyr Pro Val Thr Ser Val Leu Pro Pro Ala Ser Leu

65 70 75 80

Cys Lys Leu Ser Ser Ala Arg Trp Gly Val Cys Trp Val Asn Phe Glu

85 90 95

Ala Leu Ile Ile Thr Met Ser Val Val Gly Gly Thr Leu Leu Leu Gly  
                   100                  105                  110  
 Ile Ala Ile Cys Cys Cys Cys Cys Cys Arg Arg Lys Arg Ser Arg Lys  
                   115                  120                  125  
 Pro Asp Arg Ser Glu Glu Lys Ala Met Arg Glu Arg Glu Glu Arg Arg  
                   130                  135                  140  
 Ile Arg Gln Glu Glu Arg Arg Ala Glu Met Lys Thr Arg His Asp Glu  
 145                  150                  155                  160  
 Ile Arg Lys Lys Tyr Gly Leu Phe Lys Glu Glu Asn Pro Tyr Ala Arg  
                   165                  170                  175  
 Phe Glu Asn Asn  
                   180

<210> 59

<211> 3217

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (469).. (1875)

<400> 59

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 ctccctgttt ccttccctgt ccttcccagc lcacgctctc ttcccttgcg gcttgccttt 180  
 cttttttcct ttttttgcatt tggcgctctg gggcgtttac acacacgcgc gctgtccatt 240  
 gcagcttaca taaaggcggg cgcgattatg caattatatt gttagcgaia ttccaagagc 300  
 aatggctcgt tttcttagga ttccaacacg aaggcatcat gcatttttga aaaactagta 360

tigagaataa tacctigcaa cgtaaagaat gttttttggt atttttacac aatctctact 420  
 ttgaccaaac gagtciggac agttttcttt taatggaaaa taggagaa atg gag gaa 477

Met Glu Glu

1

aga atg gaa atg att tct gaa agg cca aaa gag agt atg tat tcc tgg 525  
 Arg Met Glu Met Ile Ser Glu Arg Pro Lys Glu Ser Met Tyr Ser Trp

5

10

15

aac aaa act gca gag aaa agt gat ttt gaa gct gta gaa gca ctt atg 573  
 Asn Lys Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu Ala Leu Met

20

25

30

35

tca atg agc tgc agt tgg aag tct gat ttt aag aaa tac gtt gaa aac 621  
 Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr Val Glu Asn

40

45

50

aga cct gtt aca cca gta tct gat ttg tca gag gaa gag aat ctg ctt 669  
 Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu Asn Leu Leu

55

60

65

ccg gga aca cct gat ttt cat aca atc cca gca ttt tgt ttg act cca 717  
 Pro Gly Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys Leu Thr Pro

70

75

80

cct tac agt cct tct gac ttt gaa ccc tct caa gtg tca aat ctg atg 765  
 Pro Tyr Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser Asn Leu Met

85

90

95

gca cca gcg cca tct act gta cac ttc aag tca ctc tca gat act gcc 813  
 Ala Pro Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser Asp Thr Ala

100

105

110

115

aaa cct cac att gcc gca cct ttc aaa gag gaa gaa aag agc cca gta 861  
 Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys Ser Pro Val



120	125	130	
tct gcc ccc aaa ctc ccc aaa gct cag gca aca agt gtg att cgt cat			909
Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His			
135	140	145	
aca gct gat gcc cag cta tgt aac cac cag acc tgc cca atg aaa gca			957
Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro Met Lys Ala			
150	155	160	
gcc agc atc ctc aac tat cag aac aat tct ttt aga aga aga acc cac			1005
Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg Arg Thr His			
165	170	175	
cta aat gtt gag gct gca aga aag aac ata cca tgt gcc gct gtg tca			1053
Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala Ala Val Ser			
180	185	190	195
cca aac aga tcc aaa tgt gag aga aac aca gtg gca gat gtt gat gag			1101
Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp Val Asp Glu			
200	205	210	
aaa gca agt gct gca ctt tat gac ttt tct gtg cct tcc tca gag acg			1149
Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser Ser Glu Thr			
215	220	225	
gtc atc tgc agg tct cag cca gcc cct gtg tcc cca caa cag aag tca			1197
Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln Gln Lys Ser			
230	235	240	
gtg ttg gtc tct cca cct gca gta tct gca ggg gga gtg cca cct atg			1245
Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val Pro Pro Met			
245	250	255	
ccg gtc atc tgc cag atg gtt ccc ctt cct gcc aac aac cct gtt gtg			1293



Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala  
 405 410 415  
 tgc ccc atg tgt gac cgg cgg ttc atg agg agt gac cat ttg acc aag 1773  
 Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys  
 420 425 430 435  
 cat gcc cgg cgc cat cta tca gcc aag aag cta cca aac tgg cag atg 1821  
 His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met  
 440 445 450  
 gaa gtg agc aag cta aat gac att gct cta cct cca acc cct gct ccc 1869  
 Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Pro  
 455 460 465  
 aca cag tgacagaccg gaaagtgaag agtcagaact aactttgggtc tcagcgggag 1925  
 Thr Gln  
 ccagtggtga tgtaaaaatg ctccactgc aagtctgtgg cccacaacg tggcttaaag 1985  
 cagaagcccc acagcctggc acgaaggccc cgtctgggtt aggtgactaa aagggttcg 2045  
 gccacaggca ggtcacagaa aggcaggttt catttctat cacataagag agatgagaaa 2105  
 gcttttattc ctttgaatat tttttgaagg ttccagatga ggtcaacaca ggtagcacag 2165  
 attttgaatc tgtgtgcata ttgtttactt tactttttgc tgtttatact tgagaccaac 2225  
 ttttcaatgt gattcttcta aagcactggg ttcaagaata tggaggctgg aaggaaataa 2285  
 acattacggt acagacatgg agatgtaaaa tgagtltgta ttattacaaa tatgtcatc 2345  
 tttttctaga gttatcttct ttattattcc tagtcttcc agtcaacatc gtggatgtag 2405  
 tgattaaata tatctagaac tatcatTTTT acactatgtt gaatatTTGG aatgaacga 2465  
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 alagctacaa ttgtttttg catttttgtt ttgaaagttt aacaaatgac tgtatctagg 2585  
 catttcattt tgctttgaac tttagtttgc ctgcagtttc ttgtgtagat ttgaaaattg 2645  
 tataccaacg tgttttctgt agactctaag atacactgca ctttgttttag aaaaaaaact 2705

gaagatgaaa tatataattgt aaagaaggga tattaagaat cttagataac ttcttgaaaa 2765  
 agatggctta tgcatacagc aaaglacctc catgttatga ggatataatg tgtgcttcat 2825  
 tgaattagaa aattagtgac cattattcac aggiggacaa atgttgicct gtttaatttat 2885  
 aggagttttt tgggatgtgg aggtagtigg gtagaaaaat tattagaaca ttacattttg 2945  
 ttaacagiat ttctctttta ttctgttata tagtggatga tatacacagt ggcaaaacaa 3005  
 aagtacattg cttaaaatat atagtgaaaa atgtcactat atcttcccat ttaacattgt 3065  
 ttttgtatat tgggtgtaga ttcttgacat caaaacttgg acccttggaa aacaaaagtt 3125  
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<210> 60

<211> 469

<212> PRT

<213> Homo sapiens

<400> 60

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Tyr	Ser	Trp	Asn	Lys	Thr	Ala	Glu	Lys	Ser	Asp	Phe	Glu	Ala	Val	Glu
				20							25				30
Ala	Leu	Met	Ser	Met	Ser	Cys	Ser	Trp	Lys	Ser	Asp	Phe	Lys	Lys	Tyr
				35							40				45
Val	Glu	Asn	Arg	Pro	Val	Thr	Pro	Val	Ser	Asp	Leu	Ser	Glu	Glu	Glu
				50							55				60
Asn	Leu	Leu	Pro	Gly	Thr	Pro	Asp	Phe	His	Thr	Ile	Pro	Ala	Phe	Cys
				65							70				75
Leu	Thr	Pro	Pro	Tyr	Ser	Pro	Ser	Asp	Phe	Glu	Pro	Ser	Gln	Val	Ser
				85							90				95

Asn	Leu	Met	Ala	Pro	Ala	Pro	Ser	Thr	Val	His	Phe	Lys	Ser	Leu	Ser
		100						105						110	
Asp	Thr	Ala	Lys	Pro	His	Ile	Ala	Ala	Pro	Phe	Lys	Glu	Glu	Glu	Lys
		115				120						125			
Ser	Pro	Val	Ser	Ala	Pro	Lys	Leu	Pro	Lys	Ala	Gln	Ala	Thr	Ser	Val
		130				135						140			
Ile	Arg	His	Thr	Ala	Asp	Ala	Gln	Leu	Cys	Asn	His	Gln	Thr	Cys	Pro
145					150					155				160	
Met	Lys	Ala	Ala	Ser	Ile	Leu	Asn	Tyr	Gln	Asn	Asn	Ser	Phe	Arg	Arg
				165					170					175	
Arg	Thr	His	Leu	Asn	Val	Glu	Ala	Ala	Arg	Lys	Asn	Ile	Pro	Cys	Ala
			180						185					190	
Ala	Val	Ser	Pro	Asn	Arg	Ser	Lys	Cys	Glu	Arg	Asn	Thr	Val	Ala	Asp
		195					200						205		
Val	Asp	Glu	Lys	Ala	Ser	Ala	Ala	Leu	Tyr	Asp	Phe	Ser	Val	Pro	Ser
		210					215						220		
Ser	Glu	Thr	Val	Ile	Cys	Arg	Ser	Gln	Pro	Ala	Pro	Val	Ser	Pro	Gln
225					230					235				240	
Gln	Lys	Ser	Val	Leu	Val	Ser	Pro	Pro	Ala	Val	Ser	Ala	Gly	Gly	Val
			245						250					255	
Pro	Pro	Met	Pro	Val	Ile	Cys	Gln	Met	Val	Pro	Leu	Pro	Ala	Asn	Asn
			260						265					270	
Pro	Val	Val	Thr	Thr	Val	Val	Pro	Ser	Thr	Pro	Pro	Ser	Gln	Pro	Pro
		275							280					285	
Ala	Val	Cys	Pro	Pro	Val	Val	Phe	Met	Gly	Thr	Gln	Val	Pro	Lys	Gly
		290					295							300	
Ala	Val	Met	Phe	Val	Val	Pro	Gln	Pro	Val	Val	Gln	Ser	Ser	Lys	Pro

305	310	315	320
Pro Val Val Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala			
	325	330	335
Pro Gly Phe Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser			
	340	345	350
Ser Arg Ile Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr			
	355	360	365
Tyr Phe Lys Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly			
	370	375	380
Glu Lys Pro Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala			
385	390	395	400
Arg Ser Asp Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys			
	405	410	415
Lys Phe Ala Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His			
	420	425	430
Leu Thr Lys His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn			
	435	440	445
Trp Gln Met Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr			
	450	455	460
Pro Ala Pro Thr Gln			

465

<210> 61

<211> 1428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125).. (868)

<400> 61

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gctctgccgt gcgctaggct tggtaggaag gcctgttcctc ggtccgcgc tttcgtcac 120  
cgcc atg tcg gga ggt ggt gtg att cgt ggc ccc gca ggg aac aac gat 169

Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp

1 5 10 15

tgc cgc atc tac gtg ggt aac tta cct cca gac atc cga acc aag gac 217

Cys Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp

20 25 30

att gag gac gtg ttc tac aaa tac ggc gct atc cgc gac atc gac ctg 265

Ile Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu

35 40 45

aag aat cgc cgc ggg gga ccg ccc ttc gcc ttc gtt gag ttc gag gac 313

Lys Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp

50 55 60

ccg cga gac gcg gaa gac gcg gtg tat ggt cgc gac ggc tat gat tac 361

Pro Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr

65 70 75

gat ggg tac cgt ctg cgg gtg gag ttt cct cga agc ggc cgt gga aca 409

Asp Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr

80 85 90 95

ggc cga ggc ggc ggc ggg ggt gga ggt ggc gga gct ccc cga ggt cgc 457

Gly Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg

100 105 110

tat ggc ccc cca tcc agg cgg tct gaa aac aga gtg gtt gtc tct gga	505
Tyr Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly	
115 120 125	
ctg cct cca agt gga agt tgg cag gat tta aag gat cac atg cgt gaa	553
Leu Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu	
130 135 140	
gca ggt gat gta tgt tat gct gat gtt tac cga gat ggc act ggt gtc	601
Ala Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val	
145 150 155	
gtg gag ttt gta cgg aaa gaa gat atg acc tat gca gtt cga aaa ctg	649
Val Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu	
160 165 170 175	
gat aac act aag ttt aga tct cat gag gga gaa act gcc tac atc cgg	697
Asp Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg	
180 185 190	
gtt aaa gtt gat ggg ccc aga agt cca agt tat gga aga tct cga tct	745
Val Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser	
195 200 205	
cga agc cgt agt cgt agc aga agc cgt agc aga agc aac agc agg agt	793
Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser	
210 215 220	
cgc agt tac tcc cca agg aga agc aga gga tca cca cgc tat tct ccc	841
Arg Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro	
225 230 235	
cgt cat agc aga tct cgc tct cgt aca taagaatgatt ggtgacactt	888
Arg His Ser Arg Ser Arg Ser Arg Thr	
240 245	



ttgtlagaac ccatgttgta tacagttttc ctttattcag tacaatcttt tcatttttta 948  
 attcaaactg tttgttcag aatgggctaa agtgttgaat tgcattcttg taatatcccc 1008  
 ttgtctcctaa catctacatt cccctcggtg ctttgataaa ttgtatttta agtgaigtca 1068  
 tagacaggat tgtttaaatt tagttaactc catactcttc agactgtgat attgtgtaaa 1128  
 tgtctatctg cccctggttg tgtgaactgg gatgttgggg gtgtttgtgg ttatcttacc 1188  
 tggggaagtt cttatgttta tcttgctttt catgtgcttt tctgtagaca tatctgaaga 1248  
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 gtcaaaagga ggattgagga ggatcagatc aataatggag gcaatggtat gactccaagt 1368  
 gctattgtca cagatgaaat tggcagtatt gacctatatac taaaaggcag gggctaaaaa 1428

<210> 62

<211> 248

<212> PRT

<213> Homo sapiens

<400> 62

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Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp Ile

20 25 30

Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu Lys

35 40 45

Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp Pro

50 55 60

Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr Asp

65 70 75 80

Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr Gly

85 90 95

Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg Tyr  
 100 105 110  
 Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly Leu  
 115 120 125  
 Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu Ala  
 130 135 140  
 Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val Val  
 145 150 155 160  
 Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu Asp  
 165 170 175  
 Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg Val  
 180 185 190  
 Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser Arg  
 195 200 205  
 Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser Arg  
 210 215 220  
 Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro Arg  
 225 230 235 240  
 His Ser Arg Ser Arg Ser Arg Thr  
 245

<210> 63

<211> 3664

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (195).. (1943)

<400> 63

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ccccaggact tctgtgactc ctgggccaca gaggtccaac cagggttaagg gccitgggat 120  
acccccigcc tggccccctt gccc aaactg gcaggggggc caggctgggc agcagccct 180  
ctttcacctc aact atg gat ctc ctg ccc ccc aag ccc aag tac aat cca 230

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro

1 5 10

ctc cgg aat gag tct ctg tca tgc ctg gag gaa ggg gct tct ggg tcc 278

Leu Arg Asn Glu Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser

15 20 25

acc ccc ccg gag gag ctg cct tcc cca tca gct tca tcc ctg ggg ccc 326

Thr Pro Pro Glu Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro

30 35 40

atc ctg cct cct ctg cct ggg gac gat agt ccc act acc ctg tgc tcc 374

Ile Leu Pro Pro Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser

45 50 55 60

ttc ttc ccc cgg atg agc aac ctg agg ctg gcc aac ccg gct ggg ggg 422

Phe Phe Pro Arg Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly

65 70 75

cgc cca ggg tct aag ggg gag cca gga agg gca gct gat gat ggg gag 470

Arg Pro Gly Ser Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu

80 85 90

ggg atc gat ggg gca gcc atg cca gag tca ggc ccc cta ccc ctc ctc 518

Gly Ile Asp Gly Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu

95 100 105

cag gac atg aac aag ctg agt gga ggc ggc ggg cgc agg act cgg gtg	566
Gln Asp Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val	
110 115 120	
gaa ggg ggc cag ctt ggg ggc gag gag tgg acc cgc cac ggg agc ttt	614
Glu Gly Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe	
125 130 135 140	
gtc aat aag ccc acg cgg ggc tgg ctg cat ccc aac gac aaa gtc atg	662
Val Asn Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met	
145 150 155	
gga ccc ggg gtt tcc tac ttg gtt cgg tac atg ggt tgt gtg gag gtc	710
Gly Pro Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val	
160 165 170	
ctc cag tca atg cgt gcc ctg gac ttc aac acc cgg act cag gtc acc	758
Leu Gln Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr	
175 180 185	
agg gag gcc atc agt ctg gtg tgt gag gct gtg ccg ggt gct aag ggg	806
Arg Glu Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly	
190 195 200	
gcg aca agg agg aga aag ccc tgt agc cgc ccg ctc agc tct atc ctg	854
Ala Thr Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu	
205 210 215 220	
ggg agg agt aac ctg aaa ttt gct gga atg cca atc act ctc acc gtc	902
Gly Arg Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val	
225 230 235	
tcc acc agc agc ctc aac ctc atg gcc gca gac tgc aaa cag atc atc	950
Ser Thr Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile	
240 245 250	

gcc aac cac cac atg caa tct atc tca ttt gca tcc ggc ggg gat ccg	998
Ala Asn His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro	
255	260
265	
gac aca gcc gag tat gtc gcc tat gtt gcc aaa gac cct gtg aat cag	1046
Asp Thr Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln	
270	275
280	
aga gcc tgc cac att ctg gag tgt ccc gaa ggg ctt gcc cag gat gtc	1094
Arg Ala Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val	
285	290
295	300
atc agc acc att ggc cag gcc ttc gag ttg cgc ttc aaa caa tac ctc	1142
Ile Ser Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu	
305	310
315	
agg aac cca ccc aaa ctg gtc acc cct cat gac agg atg gct ggc ttt	1190
Arg Asn Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe	
320	325
330	
gat ggc tca gca tgg gat gag gag gag gaa gag cca cct gac cat cag	1238
Asp Gly Ser Ala Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln	
335	340
345	
tac tat aat gac ttc ccg ggg aag gaa ccc ccc ttg ggg ggg gtg gta	1286
Tyr Tyr Asn Asp Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val	
350	355
360	
gac atg agg ctt cgg gaa gga gcc gct cca ggg gct gct cga ccc act	1334
Asp Met Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr	
365	370
375	380
gca ccc aat gcc cag acc ccc agc cac ttg gga gct aca ttg cct gta	1382
Ala Pro Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val	

385	390	395	
gga cag cct gtt ggg gga gat cca gaa gtc cgc aaa cag atg cca cct			1430
Gly Gln Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro			
400	405	410	
cca cca ccc tgt cca ggc aga gag ctt ttt gat gat ccc tcc tat gtc			1478
Pro Pro Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val			
415	420	425	
aac gtc cag aac cta gac aag gcc cgg caa gca gtg ggt ggt gct ggg			1526
Asn Val Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly			
430	435	440	
ccc ccc aat cct gct atc aat ggc agt gca ccc cgg gac ctg ttt gac			1574
Pro Pro Asn Pro Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp			
445	450	455	460
atg aag ccc ttc gaa gat gct ctt cgg gtg cct cca cct ccc cag tcg			1622
Met Lys Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser			
465	470	475	
gtg tcc atg gct gag cag ctc cga ggg gag ccc tgg ttc cat ggg aag			1670
Val Ser Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys			
480	485	490	
ctg agc cgg cgg gag gct gag gca ctg ctg cag ctc aat ggg gac ttc			1718
Leu Ser Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe			
495	500	505	
ttg gta cgg gag agc acg acc aca cct ggc cag tat gtg ctc act ggc			1766
Leu Val Arg Glu Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly			
510	515	520	
ttg cag agt ggg cag cct aag cat ttg cta ctg gtg gac cct gag ggt			1814
Leu Gln Ser Gly Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly			

525	530	535	540	
gtg gtt cgg act aag gat cac cgc ttt gaa agt gtc agt cac ctt atc				1862
Val Val Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile				
	545	550	555	
agc tac cac atg gac aat cac ttg ccc atc atc tct gcg ggc agc gaa				1910
Ser Tyr His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu				
	560	565	570	
ctg tgt cta cag caa cct gtg gag cgg aaa ctg tgatctgccc tagcgctctc				1963
Leu Cys Leu Gln Gln Pro Val Glu Arg Lys Leu				
	575	580		
ttccagaaga tgccttccaa tcccttccac cctattccct aactctcggg acctcgtttg				2023
ggagtggttct gtgggcttgg ccttggtgca gagctgggag tagcatggac tctgggtttc				2083
atatccagct gaggtagagg gtttgagtca aaagcctggg tgagaatcct gcctctcccc				2143
aaacattaat caccaaagta ttaatgtaca gaggggcccc tcacctgggc ctttcctgtg				2203
ccaacctgat gccccttccc caagaagggtg agtgcttgtc atggaaaatg tcctgtggtg				2263
acaggcccag tggaacagtc acccttctgg gcaaggggga acaaatcaca cctctgggct				2323
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gaccatctct taggtctaata gatattttat gcaaacagtt ctgggacccc tgaattcttc				2443
aatgacaggg atgccaacac ctcttgggt tctgggacct gtgttcttgc tgagcacct				2503
ctccggtttg ggttgggata acagaggcag gaggggcagc tgtccctct ccttggggat				2563
atgcaacct tagagattgc ccagagccc cactccggc caggcgggag atggaccct				2623
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ggcctcttgt acagttaact ctcccaggtg gattttgtgg aggtgagaaa aggggcattg				2863
agactataaa gcagtagaca atccccacat accatctgta gatttggaac tgcattcttt				2923

taaagtittta tatgcatata ttttagggct gctagactta ctttcctatt ttcitttcca 2983  
 ttgcctattc ttgagcacia aatgataalc aattattaca tttatacatc accittttga 3043  
 cttttccaag cccittttaca gctcttggca ttttccctgc ctaggccctgt gaggttaactg 3103  
 ggatcgcacc ttttatacca gagacctgag gcagatgaaa tttatttcca tctaggacta 3163  
 gaaaaacttg ggctctcttac cgcgagactg agaggcagaa gtcagcccga atgccctigca 3223  
 gtttcaigga ggggaaacgc aaaacctgca gtccctgagt accitttaca ggcccggccc 3283  
 agcctaggcc cgggggtggcc acaccacagc aagccggccc cccctctttt ggccttgtgg 3343  
 ataagggaga gttagccgtt ttcattccgg cctccttttg ctgtttggat gtttccacgg 3403  
 gtctcactta taccaaaggg aaaactcttc attaaagtcc gtatttcttc taaaaaaaaa 3463  
 aaaaaaaaaa tacatttata catcaccttt ttgacttttc caagcccttt tacagctctt 3523  
 ggcatitttc tcgcctaggc ctgtgaggia actgggatcg caccitttat accagagacc 3583  
 tgaggcagat gaaatttatt tccatctagg actagaaaaa ctggggcttc ttaccgcgag 3643  
 actgagaggc agaagtcagc c 3664

<210> 64

<211> 583

<212> PRT

<213> *Homo sapiens*

<400> 64

Met	Asp	Leu	Leu	Pro	Pro	Lys	Pro	Lys	Tyr	Asn	Pro	Leu	Arg	Asn	Glu
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Ser	Leu	Ser	Ser	Leu	Glu	Glu	Gly	Ala	Ser	Gly	Ser	Thr	Pro	Pro	Glu
				20						25					30
Glu	Leu	Pro	Ser	Pro	Ser	Ala	Ser	Ser	Leu	Gly	Pro	Ile	Leu	Pro	Pro
				35						40					45
Leu	Pro	Gly	Asp	Asp	Ser	Pro	Thr	Thr	Leu	Cys	Ser	Phe	Phe	Pro	Arg
				50						55					60



Met	Ser	Asn	Leu	Arg	Leu	Ala	Asn	Pro	Ala	Gly	Gly	Arg	Pro	Gly	Ser
65					70					75					80
Lys	Gly	Glu	Pro	Gly	Arg	Ala	Ala	Asp	Asp	Gly	Glu	Gly	Ile	Asp	Gly
				85						90					95
Ala	Ala	Met	Pro	Glu	Ser	Gly	Pro	Leu	Pro	Leu	Leu	Gln	Asp	Met	Asn
			100						105					110	
Lys	Leu	Ser	Gly	Gly	Gly	Gly	Arg	Arg	Thr	Arg	Val	Glu	Gly	Gly	Gln
			115					120					125		
Leu	Gly	Gly	Glu	Glu	Trp	Thr	Arg	His	Gly	Ser	Phe	Val	Asn	Lys	Pro
			130					135				140			
Thr	Arg	Gly	Trp	Leu	His	Pro	Asn	Asp	Lys	Val	Met	Gly	Pro	Gly	Val
145					150					155					160
Ser	Tyr	Leu	Val	Arg	Tyr	Met	Gly	Cys	Val	Glu	Val	Leu	Gln	Ser	Met
				165						170					175
Arg	Ala	Leu	Asp	Phe	Asn	Thr	Arg	Thr	Gln	Val	Thr	Arg	Glu	Ala	Ile
				180						185					190
Ser	Leu	Val	Cys	Glu	Ala	Val	Pro	Gly	Ala	Lys	Gly	Ala	Thr	Arg	Arg
			195							200					205
Arg	Lys	Pro	Cys	Ser	Arg	Pro	Leu	Ser	Ser	Ile	Leu	Gly	Arg	Ser	Asn
			210							215					220
Leu	Lys	Phe	Ala	Gly	Met	Pro	Ile	Thr	Leu	Thr	Val	Ser	Thr	Ser	Ser
225					230					235					240
Leu	Asn	Leu	Met	Ala	Ala	Asp	Cys	Lys	Gln	Ile	Ile	Ala	Asn	His	His
				245						250					255
Met	Gln	Ser	Ile	Ser	Phe	Ala	Ser	Gly	Gly	Asp	Pro	Asp	Thr	Ala	Glu
				260						265					270
Tyr	Val	Ala	Tyr	Val	Ala	Lys	Asp	Pro	Val	Asn	Gln	Arg	Ala	Cys	His

275	280	285	
Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile			
290	295	300	
Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro			
305	310	315	320
Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala			
325	330	335	
Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp			
340	345	350	
Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu			
355	360	365	
Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro Asn Ala			
370	375	380	
Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln Pro Val			
385	390	395	400
Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro Pro Cys			
405	410	415	
Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val Gln Asn			
420	425	430	
Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro Asn Pro			
435	440	445	
Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe			
450	455	460	
Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser Met Ala			
465	470	475	480
Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg			

	485	490	495
Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu			
500	505	510	
Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly			
515	520	525	
Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr			
530	535	540	
Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met			
545	550	555	560
Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln			
565	570	575	
Gln Pro Val Glu Arg Lys Leu			
580			

<210> 65

<211> 2493

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (41).. (1237)

<400> 65

actgcgactc gagacagcgg cccggcagga cagctccaga atg aaa atg cgg ttc 55

Met Lys Met Arg Phe

1 5

ttg ggg ttg gtg gtc tgt ttg gtt ctc tgg ccc ctg cat tct gag ggg 103

Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro Leu His Ser Glu Gly

10	15	20	
tct gga ggg aaa ctg aca gct gtg gat cct gaa aca aac atg aat gtg			151
Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu Thr Asn Met Asn Val			
25	30	35	
agt gaa att atc tct tac tgg gga ttc cct agt gag gaa tac cta gtt			199
Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser Glu Glu Tyr Leu Val			
40	45	50	
gag aca gaa gat gga tat att ctg tgc ctt aac cga att cct cat ggg			247
Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn Arg Ile Pro His Gly			
55	60	65	
agg aag aac cat tct gac aaa ggt ccc aaa cca gtt gtc ttc ctg caa			295
Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro Val Val Phe Leu Gln			
70	75	80	85
cat ggc ttg ctg gca gat tct agt aac tgg gtc aca aac ctt gcc aac			343
His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val Thr Asn Leu Ala Asn			
90	95	100	
agc agc ctg ggc ttc att ctt gct gat gct ggt ttt gac gtg tgg atg			391
Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp Val Trp Met			
105	110	115	
ggc aac agc aga gga aat acc tgg tct cgg aaa cat aag aca ctc tca			439
Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Lys Thr Leu Ser			
120	125	130	
gtt tct cag gat gaa ttc tgg gct ttc agt tat gat gag atg gca aaa			487
Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu Met Ala Lys			
135	140	145	
tat gac cta cca gct tcc att aac ttc att ctg aat aaa act ggc caa			535
Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu Asn Lys Thr Gly Gln			

150	155	160	165	
gaa caa gtg tat tat gtg ggt cat tct caa ggc acc act ata ggt ttt				583
Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly Thr Thr Ile Gly Phe				
	170	175	180	
ata gca ttt tca cag atc cct gag ctg gct aaa agg att aaa atg ttt				631
Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys Arg Ile Lys Met Phe				
	185	190	195	
ttt gcc ctg ggt cct gtg gct tcc gtc gcc ttc tgt act agc cct atg				679
Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe Cys Thr Ser Pro Met				
	200	205	210	
gcc aaa tta gga cga tta cca gat cat ctc att aag gac tta ttt gga				727
Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile Lys Asp Leu Phe Gly				
	215	220	225	
gac aaa gaa ttt ctt ccc cag agt gcg ttt ttg aag tgg ctg ggt acc				775
Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu Lys Trp Leu Gly Thr				
	230	235	240	245
cac gtt tgc act cat gtc ata ctg aag gag ctc tgt gga aat ctc tgt				823
His Val Cys Thr His Val Ile Leu Lys Glu Leu Cys Gly Asn Leu Cys				
	250	255	260	
ttt ctt ctg tgt gga ttt aat gag aga aat tta aat atg tct aga gtg				871
Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu Asn Met Ser Arg Val				
	265	270	275	
gat gla tat aca aca cat tct cct gct gga act tct gtg caa aac atg				919
Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr Ser Val Gln Asn Met				
	280	285	290	
tta cac tgg agc cag gct gtt aaa ttc caa aag ttt caa gcc ttt gac				967

Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys Phe Gln Ala Phe Asp  
 295 300 305  
 tgg gga agc agt gcc aag aat tat ttt cat tac aac cag agt tat cct 1015  
 Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr Asn Gln Ser Tyr Pro  
 310 315 320 325  
 ccc aca tac aat gtg aag gac atg ctt gtg ccg act gca gtc tgg agc 1063  
 Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro Thr Ala Val Trp Ser  
 330 335 340  
 ggg ggt cac gac tgg ctt gca gat gtc tac gac gtc aat atc tta ctg 1111  
 Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp Val Asn Ile Leu Leu  
 345 350 355  
 act cag atc acc aac ttg gtg ttc cat gag agc att ccg gaa tgg gag 1159  
 Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser Ile Pro Glu Trp Glu  
 360 365 370  
 cat ctt gac ttc att tgg ggc ctg gat gcc cct tgg agg ctt tat aat 1207  
 His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro Trp Arg Leu Tyr Asn  
 375 380 385  
 aaa att att aat cta atg agg aaa tat cag tgaaagctgg acttgagctg 1257  
 Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln  
 390 395  
 tgtaccacca agtcaatgat tatgtcatgt gaaaatgtgt ttgcttcatt tctgtaaaac 1317  
 acttgttttt ctttcccagg tcttttgttt ttttataacc aagaaaatga taactttgaa 1377  
 gatgcccagt tcactctagt ttcaattaga aacatactag ctattttttc ttttaattagg 1437  
 gctggaatag gaagccagtg tctcaacat agtattgtct ctttaagtct tttaaataic 1497  
 actgatgtgt aaaaagglica ttataccat tctgttttta aaatttaaaa tatattgact 1557  
 ttttgccctt cataggacaa agtaatatat gtgttggaat tttaaaattg igtgttcatt 1617  
 ggtaaatctg tcactgactt aagcgaggta taaaagtagc cagttttcat gtccttgcc 1677

taaagagctc tctagtcctaa cggctcttgta gttagagatc taaatgacat tttatcatgt 1737  
 ttccctgcag caggctgcata gtcaaatcca gaaatatacac agctgtgccca gtaataagga 1797  
 tgctaacaat taatittatc aaacctaaact gtgacagctg tgatttgaca cgttttaatt 1857  
 gctcaggtaa aatgaaatag tttccggcg tcttcaaaaa caaatigcac tgataaaaca 1917  
 aaaacaaaag tatgttttaa atgctttgaa gactgataca ctcaaccatc tatattcatg 1977  
 agctctcaat ttcattggcag gccatagtic tacttatctg agaagcaaat ccctgtggag 2037  
 actataccac tattttttct gagattaatg tactcttgga gcccgciact gtcgttatgt 2097  
 atcacatctg tgtgaagcca aagccccgtg gttgcccattg agaagtgtcc ttgttcattt 2157  
 tcacccaaat gaagtgtgaa cgtgaigtgtt icggatgcaa actcagctca gggattcatt 2217  
 ttgtgtctta gttttataatg catccittatt tttaatcac ctccttcacg tccctatgtt 2277  
 gggaagicca tatttgtctg ctlttcttgc agcatcattt ccttacaata ctgtccgggtg 2337  
 gacaaaatga caattgatat gttttctga tataattact ttagctgcac taacagtaca 2397  
 atgcttgtaa atggttaata taggcagggc gaatactact ttgttaacttt taaagctta 2457  
 aacttttcaa taaaattgag tgagacttat aggcc 2493

<210> 66

<211> 399

<212> PRT

<213> Homo sapiens

<400> 66

Met Lys Met Arg Phe Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro

1

5

10

15

Leu His Ser Glu Gly Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu

20

25

30

Thr Asn Met Asn Val Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser

35

40

45

Glu Glu Tyr Leu Val Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn

50	55	60	
Arg Ile Pro His Gly Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro			
65	70	75	80
Val Val Phe Leu Gln His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val			
	85	90	95
Thr Asn Leu Ala Asn Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly			
	100	105	110
Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys			
	115	120	125
His Lys Thr Leu Ser Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr			
	130	135	140
Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu			
145	150	155	160
Asn Lys Thr Gly Gln Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly			
	165	170	175
Thr Thr Ile Gly Phe Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys			
	180	185	190
Arg Ile Lys Met Phe Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe			
	195	200	205
Cys Thr Ser Pro Met Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile			
	210	215	220
Lys Asp Leu Phe Gly Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu			
225	230	235	240
Lys Trp Leu Gly Thr His Val Cys Thr His Val Ile Leu Lys Glu Leu			
	245	250	255
Cys Gly Asn Leu Cys Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu			



260	265	270
Asn Met Ser Arg Val Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr		
275	280	285
Ser Val Gln Asn Met Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys		
290	295	300
Phe Gln Ala Phe Asp Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr		
305	310	315
Asn Gln Ser Tyr Pro Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro		
325	330	335
Thr Ala Val Trp Ser Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp		
340	345	350
Val Asn Ile Leu Leu Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser		
355	360	365
Ile Pro Glu Trp Glu His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro		
370	375	380
Trp Arg Leu Tyr Asn Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln		
385	390	395

<210> 67

<211> 1633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (323).. (1177)

<400> 67

aacttaatgt ttttgcaatg gactttgagt taagattatt ttttaaacc tgaggactag 60

cattaatiga cagctgaccc aggtgctaca cagaagtggga ttcagtgaat ctaggaagac 120  
 agcagcagac aggatccag gaaccagtgt ttgatgaagc taggactgag gagcaagcga 180  
 gcaagcagca gticgtggaa tccgtctgc tgcgtcttc ctggtttagg agccgacggg 240  
 cgctcgcagg ctacagcgcgc gctgccgcgc gcaggacccg gccgcctccg ccgccgccgc 300  
 cgccccctaag cctcccgaag cc atg gcc ggg ctc ggc cac ccc gcc gcc ttc 352

Met Ala Gly Leu Gly His Pro Ala Ala Phe

1 5 10

ggc cgg gcc acc cac gcc gtg gtg cgg gcg cta ccc gag tcg ctc ggc 400  
 Gly Arg Ala Thr His Ala Val Val Arg Ala Leu Pro Glu Ser Leu Gly

15 20 25

cag cac gcg ctg aga agc gcc aag ggc gag gag gtg gac gtc gcc cgc 448  
 Gln His Ala Leu Arg Ser Ala Lys Gly Glu Glu Val Asp Val Ala Arg

30 35 40

gcg gaa cgg cag cac cag ctc tac gtg ggc gtg ctg ggc agc aag ctg 496  
 Ala Glu Arg Gln His Gln Leu Tyr Val Gly Val Leu Gly Ser Lys Leu

45 50 55

ggg ctg cag gtg gtg gag ctg ccg gcc gac gag agc ctt ccg gac tgc 544  
 Gly Leu Gln Val Val Glu Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys

60 65 70

gtc ttc gtg gag gac gtg gcc gtg gtg tgc gag gag acg gcc ctc atc 592  
 Val Phe Val Glu Asp Val Ala Val Val Cys Glu Glu Thr Ala Leu Ile

75 80 85 90

acc cga ccc ggg gcg ccg agc cgg agg aag gag gtt gac atg atg aaa 640  
 Thr Arg Pro Gly Ala Pro Ser Arg Arg Lys Glu Val Asp Met Met Lys

95 100 105

gaa gca tta gaa aaa ctt cag ctc aat ala gla gag atg aaa gat gaa 688  
 Glu Ala Leu Glu Lys Leu Gln Leu Asn Ile Val Glu Met Lys Asp Glu

110	115	120	
aat gca act tta gat ggc gga gat gtt tta ttc aca ggc aga gaa ttt	736		
Asn Ala Thr Leu Asp Gly Gly Asp Val Leu Phe Thr Gly Arg Glu Phe			
125	130	135	
ttt gtg ggc ctt tcc aaa agg aca aat caa cga ggt gct gaa atc ttg	784		
Phe Val Gly Leu Ser Lys Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu			
140	145	150	
gct gat act ttt aag gac tat gca gtc tcc aca gtg cca gtg gca gat	832		
Ala Asp Thr Phe Lys Asp Tyr Ala Val Ser Thr Val Pro Val Ala Asp			
155	160	165	170
ggg ttg cat ttg aag agt ttc tgc agc atg gct ggg cct aac ctg atc	880		
Gly Leu His Leu Lys Ser Phe Cys Ser Met Ala Gly Pro Asn Leu Ile			
175	180	185	
gca att ggg tct agt gaa tct gca cag aag gcc ctt aag atc atg caa	928		
Ala Ile Gly Ser Ser Glu Ser Ala Gln Lys Ala Leu Lys Ile Met Gln			
190	195	200	
cag atg agt gac cac cgc tac gac aaa ctc act gtg cct gat gac ata	976		
Gln Met Ser Asp His Arg Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile			
205	210	215	
gca gca aac tgt ata tat cta aat atc ccc aac aaa ggg cac gtc ttg	1024		
Ala Ala Asn Cys Ile Tyr Leu Asn Ile Pro Asn Lys Gly His Val Leu			
220	225	230	
ctg cac cga acc ccg gaa gag tat cca gaa agt gca aag gtt tat gag	1072		
Leu His Arg Thr Pro Glu Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu			
235	240	245	250
aaa ctg aag gac cat atg ctg atc ccc gtg agc atg tct gaa ctg gaa	1120		

Lys Leu Lys Asp His Met Leu Ile Pro Val Ser Met Ser Glu Leu Glu  
                   255                          260                          265  
 aag gtg gat ggg ctg ctc acc tgc tgc tca gtt tta att aac aag aaa 1168  
 Lys Val Asp Gly Leu Leu Thr Cys Cys Ser Val Leu Ile Asn Lys Lys  
                   270                          275                          280  
 gia gac tcc tgagctgcag agtccccccc ggtagccggc aagaccgcac 1217  
 Val Asp Ser  
                   285  
 aggcaaggcc gatgactctg tgcccactcc tgttgttttc ctigacaatc tactgtgcca 1277  
 ctgtgctact aactcttggt tacaaaattt gattctaagt tgaattgctt cattcaacac 1337  
 cccaccctc cctccccrcg aggtggctacc taagctgtgg atttgctaaa tgaattaagc 1397  
 aacctagaag atacagagct aatgaattat caaatgtga ttaatcccag taaggaaaca 1457  
 ctcatltagt gictgtatit ttggtginaa aattatttag ttgccagtat attctgaaga 1517  
 atgtcttctt gatcagtcag ataagcttgc tttttttttt tttttttcat gaatcatgtt 1577  
 tggttccctgt gaaagtcctt ggtccaggga tcctcctcct ttctctttta cttctg 1633

<210> 68

<211> 285

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Gly Leu Gly His Pro Ala Ala Phe Gly Arg Ala Thr His Ala  
       1                  5                          10                          15  
 Val Val Arg Ala Leu Pro Glu Ser Leu Gly Gln His Ala Leu Arg Ser  
                   20                          25                          30  
 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln  
                   35                          40                          45

Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu  
 50 55 60  
 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val  
 65 70 75 80  
 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro  
 85 90 95  
 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu  
 100 105 110  
 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly  
 115 120 125  
 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys  
 130 135 140  
 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp  
 145 150 155 160  
 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser  
 165 170 175  
 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu  
 180 185 190  
 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg  
 195 200 205  
 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr  
 210 215 220  
 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu  
 225 230 235 240  
 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met  
 245 250 255  
 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu

260 265 270  
 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser

275 280 285

<210> 69

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147).. (1421)

<400> 69

aagcgccigt ctgaacctct gccagtcctg gagactggig cccigagctc caaccagcgg 60  
 gcctcatctc caccctcacc accgcaactt ctcacccgag caagaagcag ctcccagaga 120  
 gaaagaacgt tcccacctgc ctagcc atg gga gag gac gct gca cag gcc gaa 173

Met Gly Glu Asp Ala Ala Gln Ala Glu

1 5

aag ttc cag cac cct ggg tct gac atg cgg cag gaa aag ccc tcg agc 221

Lys Phe Gln His Pro Gly Ser Asp Met Arg Gln Glu Lys Pro Ser Ser

10 15 20 25

ccc agc ccg atg cct tcc tcc aca cca agc ccc agc ctg aac cta ggg 269

Pro Ser Pro Met Pro Ser Ser Thr Pro Ser Pro Ser Leu Asn Leu Gly

30 35 40

aac aca gag gag gcc atc cgg gac aac tca cag gtg aac gca gtc acg 317

Asn Thr Glu Glu Ala Ile Arg Asp Asn Ser Gln Val Asn Ala Val Thr

45 50 55

gtg ctc acg ctc ctg gac aag ctg gtg aac atg cta gac gct gtg cag 365



cic tcc tca gat gat gat tlg ccc cac gat gag gag gcc ctg gaa gac	797
Leu Ser Ser Asp Asp Asp Leu Pro His Asp Glu Glu Ala Leu Glu Asp	
205 210 215	
agt gcc gag gaa aag gtg gaa gaa agt agg gca gag aaa ata aaa aga	845
Ser Ala Glu Glu Lys Val Glu Glu Ser Arg Ala Glu Lys Ile Lys Arg	
220 225 230	
tcc agc ctg aag aaa gtg gat agc ctc aag aaa gca ttt tct cgc cag	893
Ser Ser Leu Lys Lys Val Asp Ser Leu Lys Lys Ala Phe Ser Arg Gln	
235 240 245	
aac atc gag aaa aag atg aac aag ctg ggg aca aag atc gta tct gta	941
Asn Ile Glu Lys Lys Met Asn Lys Leu Gly Thr Lys Ile Val Ser Val	
250 255 260 265	
gag agg aga gag aag att aag aaa tct ctc acg tca aat cac cag aaa	989
Glu Arg Arg Glu Lys Ile Lys Lys Ser Leu Thr Ser Asn His Gln Lys	
270 275 280	
ata tcc tca gga aaa agc tcc ccc ttc aag gtt tct ccc ctc act ttc	1037
Ile Ser Ser Gly Lys Ser Ser Pro Phe Lys Val Ser Pro Leu Thr Phe	
285 290 295	
ggg cgg aag aaa gtc cga gag gga gaa agc cat gca gaa aat gag acc	1085
Gly Arg Lys Lys Val Arg Glu Gly Glu Ser His Ala Glu Asn Glu Thr	
300 305 310	
aag tca gaa gac ctg cct agc agt gag cag atg cca aat gac cag gaa	1133
Lys Ser Glu Asp Leu Pro Ser Ser Glu Gln Met Pro Asn Asp Gln Glu	
315 320 325	
gag gag tcc ttt gca gag ggt cat tcc gaa gcg tcc ctc gcc agc gct	1181
Glu Glu Ser Phe Ala Glu Gly His Ser Glu Ala Ser Leu Ala Ser Ala	
330 335 340 345	



ctg gtg gaa ggg gaa att gca gag gag gct gct gag aag gcg acc tcc 1229  
 Leu Val Glu Gly Glu Ile Ala Glu Glu Ala Ala Glu Lys Ala Thr Ser  
 350 355 360  
 agg ggg agt aac tcg ggg atg gac agc aac atc gac ttg act att gtg 1277  
 Arg Gly Ser Asn Ser Gly Met Asp Ser Asn Ile Asp Leu Thr Ile Val  
 365 370 375  
 gaa gat gaa gag gag gag tca gtg gcc ctg gaa cag gca cag aag gta 1325  
 Glu Asp Glu Glu Glu Glu Ser Val Ala Leu Glu Gln Ala Gln Lys Val  
 380 385 390  
 cgc tat gag ggt agc tac gcg cta aca tcc gag gag gcg gag cgc tcc 1373  
 Arg Tyr Glu Gly Ser Tyr Ala Leu Thr Ser Glu Glu Ala Glu Arg Ser  
 395 400 405  
 gat ggg gac ccc gtg cag ccc gcc gtg ctc cag gtg cac cag acc tcc 1421  
 Asp Gly Asp Pro Val Gln Pro Ala Val Leu Gln Val His Gln Thr Ser  
 410 415 420 425  
 tgagcttaga gccaccgtgc catcctgtgc tgtgctcaag cgggcagcca gggctgaaga 1481  
 acaaactctt gcacatctcc agcacgactc acccactcct gcgttcctgt ccaggcagta 1541  
 atcattgacc atatagtcac agtaagacac acgagaccag gccttaccat gaaagcgacc 1601  
 tgtcacggac tccactttta atttgctctt aggttctatc tctgtagaat gtctccaaga 1661  
 ttgaagaaga aactgagcag ttgaaaaatg ctaatctctt tgacttagtc agaaaaaac 1721  
 agaggataat taagatacta gicatgaaaa gtgattcatt cttttttgtc attccatc 1779

<210> 70

<211> 425

<212> PRT

<213> Homo sapiens

<400> 70

Met	Gly	Glu	Asp	Ala	Ala	Gln	Ala	Glu	Lys	Phe	Gln	His	Pro	Gly	Ser
1				5					10					15	
Asp	Met	Arg	Gln	Glu	Lys	Pro	Ser	Ser	Pro	Ser	Pro	Met	Pro	Ser	Ser
			20					25						30	
Thr	Pro	Ser	Pro	Ser	Leu	Asn	Leu	Gly	Asn	Thr	Glu	Glu	Ala	Ile	Arg
			35					40						45	
Asp	Asn	Ser	Gln	Val	Asn	Ala	Val	Thr	Val	Leu	Thr	Leu	Leu	Asp	Lys
			50					55						60	
Leu	Val	Asn	Met	Leu	Asp	Ala	Val	Gln	Glu	Asn	Gln	His	Lys	Met	Glu
65					70					75					80
Gln	Arg	Gln	Ile	Ser	Leu	Glu	Gly	Ser	Val	Lys	Gly	Ile	Gln	Asn	Asp
					85					90					95
Leu	Thr	Lys	Leu	Ser	Lys	Tyr	Gln	Ala	Ser	Thr	Ser	Asn	Thr	Val	Ser
					100					105					110
Lys	Leu	Leu	Glu	Lys	Ser	Arg	Lys	Val	Ser	Ala	His	Thr	Arg	Ala	Val
					115					120					125
Lys	Glu	Arg	Met	Asp	Arg	Gln	Cys	Ala	Gln	Val	Lys	Arg	Leu	Glu	Asn
					130					135					140
Asn	His	Ala	Gln	Leu	Leu	Arg	Arg	Asn	His	Phe	Lys	Val	Leu	Ile	Phe
145						150					155				160
Gln	Glu	Glu	Asn	Glu	Ile	Pro	Ala	Ser	Val	Phe	Val	Lys	Gln	Pro	Val
					165					170					175
Ser	Gly	Ala	Val	Glu	Gly	Lys	Glu	Glu	Leu	Pro	Asp	Glu	Asn	Lys	Ser
					180					185					190
Leu	Glu	Glu	Thr	Leu	His	Thr	Val	Asp	Leu	Ser	Ser	Asp	Asp	Asp	Leu
					195					200					205

Pro His Asp Glu Glu Ala Leu Glu Asp Ser Ala Glu Glu Lys Val Glu  
 210 215 220  
 Glu Ser Arg Ala Glu Lys Ile Lys Arg Ser Ser Leu Lys Lys Val Asp  
 225 230 235 240  
 Ser Leu Lys Lys Ala Phe Ser Arg Gln Asn Ile Glu Lys Lys Met Asn  
 245 250 255  
 Lys Leu Gly Thr Lys Ile Val Ser Val Glu Arg Arg Glu Lys Ile Lys  
 260 265 270  
 Lys Ser Leu Thr Ser Asn His Gln Lys Ile Ser Ser Gly Lys Ser Ser  
 275 280 285  
 Pro Phe Lys Val Ser Pro Leu Thr Phe Gly Arg Lys Lys Val Arg Glu  
 290 295 300  
 Gly Glu Ser His Ala Glu Asn Glu Thr Lys Ser Glu Asp Leu Pro Ser  
 305 310 315 320  
 Ser Glu Gln Met Pro Asn Asp Gln Glu Glu Glu Ser Phe Ala Glu Gly  
 325 330 335  
 His Ser Glu Ala Ser Leu Ala Ser Ala Leu Val Glu Gly Glu Ile Ala  
 340 345 350  
 Glu Glu Ala Ala Glu Lys Ala Thr Ser Arg Gly Ser Asn Ser Gly Met  
 355 360 365  
 Asp Ser Asn Ile Asp Leu Thr Ile Val Glu Asp Glu Glu Glu Glu Ser  
 370 375 380  
 Val Ala Leu Glu Gln Ala Gln Lys Val Arg Tyr Glu Gly Ser Tyr Ala  
 385 390 395 400  
 Leu Thr Ser Glu Glu Ala Glu Arg Ser Asp Gly Asp Pro Val Gln Pro  
 405 410 415  
 Ala Val Leu Gln Val His Gln Thr Ser

&lt;210&gt; 71

&lt;211&gt; 2638

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (288).. (1844)

&lt;400&gt; 71

gaggaaaggg gaaatgcggc ccgctcccca ctcagtgcc ctcgtgcc ctcctggcca 60  
 ggccctgagg gcacccggtt gctgttcc tccgtcttc cccaaggact atcagagatg 120  
 ccagcgtgac ccctgacacg tgtgtgcagc agcctgcagc tgccccaagc catggctgaa 180  
 cactgactcc cagctgtggg ctccaccatt acagactccc cagggttca aagacttctc 240  
 agcttcgagc atggcttttg gctgtcaggg cagctgtaca atagtgg atg ttt gag 296

Met Phe Glu

1

acg gag gca gat gag aag agg gag atg gcc ttg gag gaa ggg aag ggg 344  
 Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu Gly Lys Gly

5

10

15

cct ggt gcc gag gat tcc cca ccc agc aag gag ccc tct cct ggc cag 392  
 Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser Pro Gly Gln

20

25

30

35

gag ctt cct cca gga caa gac ctt cca ccc aac aag gac tcc cct tct 440  
 Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp Ser Pro Ser

40

45

50

ggg cag gaa ccc gct ccc agc caa gaa cca ctg tcc agc aaa gac tca 488

Gly	Gln	Glu	Pro	Ala	Pro	Ser	Gln	Glu	Pro	Leu	Ser	Ser	Lys	Asp	Ser		
			55					60					65				
gct	acc	tct	gaa	gga	tcc	cct	cca	ggc	cca	gat	gct	ccg	ccc	agc	aag	536	
Ala	Thr	Ser	Glu	Gly	Ser	Pro	Pro	Gly	Pro	Asp	Ala	Pro	Pro	Ser	Lys		
			70					75					80				
gat	gtg	cca	cca	tgc	cag	gaa	ccc	cct	cca	gcc	caa	gac	ctc	tca	ccc	584	
Asp	Val	Pro	Pro	Cys	Gln	Glu	Pro	Pro	Pro	Ala	Gln	Asp	Leu	Ser	Pro		
			85					90					95				
tgc	cag	gac	cta	cct	gct	ggt	caa	gaa	ccc	ctg	cct	cac	cag	gac	cct	632	
Cys	Gln	Asp	Leu	Pro	Ala	Gly	Gln	Glu	Pro	Leu	Pro	His	Gln	Asp	Pro		
100				105						110				115			
cta	ctc	acc	aaa	gac	ctc	cct	gcc	atc	cag	gaa	tcc	ccc	acc	cgg	gac	680	
Leu	Leu	Thr	Lys	Asp	Leu	Pro	Ala	Ile	Gln	Glu	Ser	Pro	Thr	Arg	Asp		
				120					125					130			
ctt	cca	ccc	tgt	caa	gat	ctg	cct	cct	agc	cag	gtc	tcc	ctg	cca	gcc	728	
Leu	Pro	Pro	Cys	Gln	Asp	Leu	Pro	Pro	Ser	Gln	Val	Ser	Leu	Pro	Ala		
				135					140					145			
aag	gcc	ctt	act	gag	gac	acc	atg	agc	tcc	ggg	gac	cta	cta	gca	gct	776	
Lys	Ala	Leu	Thr	Glu	Asp	Thr	Met	Ser	Ser	Gly	Asp	Leu	Leu	Ala	Ala		
			150					155						160			
act	ggg	gac	cca	cct	gcg	gcc	ccc	agg	cca	gcc	ttc	gtg	atc	cct	gag	824	
Thr	Gly	Asp	Pro	Pro	Ala	Ala	Pro	Arg	Pro	Ala	Phe	Val	Ile	Pro	Glu		
			165					170						175			
gtc	cgg	ctg	gat	agc	acc	tac	agc	cag	aag	gca	ggg	gca	gag	cag	ggc	872	
Val	Arg	Leu	Asp	Ser	Thr	Tyr	Ser	Gln	Lys	Ala	Gly	Ala	Glu	Gln	Gly		
180				185						190					195		

tgc tgc gga gat gag gag gat gca gaa gag gcc gag gag gtg gag gag	920
Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu Val Glu Glu	
200 205 210	
ggg gag gaa ggg gag gag gac gag gat gag gac acc agc gat gac aac	968
Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser Asp Asp Asn	
215 220 225	
tac gga gag cgc agt gag gcc aag cgc agc agc atg atc gag acg ggc	1016
Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile Glu Thr Gly	
230 235 240	
cag ggg gct gag ggt ggc ctc tca ctg cgt gtg cag aac tcg ctg cgg	1064
Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn Ser Leu Arg	
245 250 255	
cgc cgg acg cac agc gag ggc agc ctg ctg cag gag ccc cga ggg ccc	1112
Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro Arg Gly Pro	
260 265 270 275	
tgc ttt gcc tcc gac acc acc ttg cac tgc tca gac ggt gag ggc gcc	1160
Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly Glu Gly Ala	
280 285 290	
gcc tcc acc tgg ggc atg cct tcg ccc agc acc ctc aag aaa gag ctg	1208
Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys Lys Glu Leu	
295 300 305	
ggc cgc aat ggt ggc tcc atg cac cac ctt tcc ctc ttc ttc aca gga	1256
Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe Phe Thr Gly	
310 315 320	
cac agg aag atg agc ggg gct gac acc gtt ggg gat gat gac gaa gcc	1304
His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp Asp Glu Ala	
325 330 335	



470	475	480	
gca cag aag cgc atc ttc ggg ctc atg gaa aag gac tcg tac cct cgc			1784
Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser Tyr Pro Arg			
485	490	495	
ttt ctc cgt tct gac ctc tac ctg gac ctt att aac cag aag aag atg			1832
Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln Lys Lys Met			
500	505	510	515
agt ccc ccg ctt taggggccac tggagtcgag ctcagcgttc acaccaggcg			1884
Ser Pro Pro Leu			
ggctgggtcc cctgccacc tgcctccctg cccctgtga cggagggggc aagcaagccc			1944
ccagaggccg tgtctctgga cagacggata gacatacgga agcagggcct ggaccaagag			2004
aggcccaggc tactggagga gtagaaggat gggccccgtg gggccccac tggccccgta			2064
cgagggggcc caagaccctg gcaggtcagg ggccttgcc aagccagatc tggagctgct			2124
gctccctgct gcggagaccg cggaggcttc gcgttgacca agtcccttaa agaactggct			2184
gatggggcag gaggtccagg cctgggctct cgggccctcc tagagggccca ttggagcttg			2244
cagctcagac cccactttg agttttatct atttaaata tagttggatg cttggcacgt			2304
cgtcctgtaa taggaaacc tgcctcatc agttttcctg atttacaagt gcaatatttt			2364
agccaatgcc ttgggagaag ctgccatgca aaggctggaca ccattctcca gcttcagggg			2424
atatgctcgt cccgggcacc ggtggcaggc agctggcctt ctggactaag gcagcctggg			2484
gggacactgc agtctggcta cacacagaga tctggcacc cctgggtgga gtgtccctcg			2544
ggggctttgg gaaagcatgg caccctcaga ccacacagta gccaaagtct ggagcaaata			2604
aaaggcctgt gttatttctt gtctttgaaa aaaa			2638

<210> 72

<211> 519

<212> PRT

<213> Homo sapiens



<400> 72

Met Phe Glu Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu

1 5 10 15

Gly Lys Gly Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser

20 25 30

Pro Gly Gln Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp

35 40 45

Ser Pro Ser Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser

50 55 60

Lys Asp Ser Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro

65 70 75 80

Pro Ser Lys Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp

85 90 95

Leu Ser Pro Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His

100 105 110

Gln Asp Pro Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro

115 120 125

Thr Arg Asp Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser

130 135 140

Leu Pro Ala Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu

145 150 155 160

Leu Ala Ala Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val

165 170 175

Ile Pro Glu Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala

180 185 190

Glu Gln Gly Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu

195 200 205

Val	Glu	Glu	Gly	Glu	Glu	Gly	Glu	Glu	Asp	Glu	Asp	Glu	Asp	Thr	Ser
210						215						220			
Asp	Asp	Asn	Tyr	Gly	Glu	Arg	Ser	Glu	Ala	Lys	Arg	Ser	Ser	Met	Ile
225						230					235			240	
Glu	Thr	Gly	Gln	Gly	Ala	Glu	Gly	Gly	Leu	Ser	Leu	Arg	Val	Gln	Asn
					245				250					255	
Ser	Leu	Arg	Arg	Arg	Thr	His	Ser	Glu	Gly	Ser	Leu	Leu	Gln	Glu	Pro
					260				265					270	
Arg	Gly	Pro	Cys	Phe	Ala	Ser	Asp	Thr	Thr	Leu	His	Cys	Ser	Asp	Gly
					275				280					285	
Glu	Gly	Ala	Ala	Ser	Thr	Trp	Gly	Met	Pro	Ser	Pro	Ser	Thr	Leu	Lys
					290				295					300	
Lys	Glu	Leu	Gly	Arg	Asn	Gly	Gly	Ser	Met	His	His	Leu	Ser	Leu	Phe
305						310					315			320	
Phe	Thr	Gly	His	Arg	Lys	Met	Ser	Gly	Ala	Asp	Thr	Val	Gly	Asp	Asp
						325					330			335	
Asp	Glu	Ala	Ser	Arg	Lys	Arg	Lys	Ser	Lys	Asn	Leu	Ala	Lys	Asp	Met
					340						345			350	
Lys	Asn	Lys	Leu	Gly	Ile	Phe	Arg	Arg	Arg	Asn	Glu	Ser	Pro	Gly	Ala
					355						360			365	
Pro	Pro	Ala	Gly	Lys	Ala	Asp	Lys	Met	Met	Lys	Ser	Phe	Lys	Pro	Thr
					370						375			380	
Ser	Glu	Glu	Ala	Leu	Lys	Trp	Gly	Glu	Ser	Leu	Glu	Lys	Leu	Leu	Val
385						390					395			400	
His	Lys	Tyr	Gly	Leu	Ala	Val	Phe	Gln	Ala	Phe	Leu	Arg	Thr	Glu	Phe
					405						410			415	

Ser Glu Glu Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys

420

425

430

Val Lys Ser Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala

435

440

445

Glu Tyr Ile Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr

450

455

460

Thr Arg Glu His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys

465

470

475

480

Phe Asp Leu Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser

485

490

495

Tyr Pro Arg Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln

500

505

510

Lys Lys Met Ser Pro Pro Leu

515

<210> 73

<211> 1901

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (250).. (1206)

<400> 73

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tggaatgaaa attcacctgc cctgagttg gctcctaattg ggggtgggag tgttacttcg 120  
gttcccaggt tggaagatta tctcaccggg ccccagctat ataagctgac cgggtgtggag 180  
gggcccagca gggccaactc cagggatcc ttcacgaca gaaaaacata caagactcct 240

tcagccaac atg atg gta ctg aaa gta gag gaa ctg gtc act gga aag aag 291

Met Met Val Leu Lys Val Glu Glu Leu Val Thr Gly Lys Lys

1 5 10

aat ggc aat ggg gag gca ggg gaa ttc ctt cct gag gat ttc aga gat 339

Asn Gly Asn Gly Glu Ala Gly Glu Phe Leu Pro Glu Asp Phe Arg Asp

15 20 25 30

gga gag tat gaa gct gct gtt act tta gag aag cag gag gat ctg aag 387

Gly Glu Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys

35 40 45

aca ctt cta gcc cac cct gtg acc ctg ggg gag caa cag tgg aaa agc 435

Thr Leu Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser

50 55 60

gag aaa caa cga gag gca gag ctc cca aag aaa aaa cta gaa caa aga 483

Glu Lys Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg

65 70 75

tcc aag ctt gaa aat tta gaa gac ctt gaa ata atc att caa ctg aag 531

Ser Lys Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys

80 85 90

aaa agg aaa aaa tac agg aaa act aaa gtt cca gtt gta aag gaa cca 579

Lys Arg Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro

95 100 105 110

gaa cct gaa atc att acg gaa cct gtg gat gtg cct acg ttt ctg aag 627

Glu Pro Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys

115 120 125

gct gct ctg gag aat aaa ctg cca gta gta gaa aaa ttc ttg tca gac 675

Ala Ala Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp

130 135 140

aag aac aat cca gat gtt tgt gat gag tat aaa cgg aca gct ctt cat	723
Lys Asn Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His	
145 150 155	
aga gca tgc ttg gaa gga cat ttg gca att gtg gag aag tta atg gaa	771
Arg Ala Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu	
160 165 170	
gct gga gcc cag atc gaa ttc cgt gat atg ctt gaa tcc aca gcc atc	819
Ala Gly Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile	
175 180 185 190	
cac tgg gca agc cgt gga gga aac ctg gat gtt tta aaa ttg ttg ctg	867
His Trp Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu	
195 200 205	
aat aaa gga gca aaa att agc gcc cga gat aag ttg ctc agc aca gcg	915
Asn Lys Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala	
210 215 220	
ctg cat gtg gcg gtg agg act ggc cac tat gag tgc gcg gag cat ctt	963
Leu His Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu	
225 230 235	
atc gcc tgt gag gca gac ctc aac gcc aaa gac aga gaa gga gat acc	1011
Ile Ala Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr	
240 245 250	
ccg ttg cat gat gcg gtg aga ctg aac cgc tat aag atg atc cga ctc	1059
Pro Leu His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu	
255 260 265 270	
ctg att atg tat ggc gcg gat ctc aac atc aag aac tgt gct ggg aag	1107
Leu Ile Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys	

275	280	285	
acg ccg atg gat ctg gtg cta cac tgg cag aat gga acc aaa gca ata			1155
Thr Pro Met Asp Leu Val Leu His Trp Gln Asn Gly Thr Lys Ala Ile			
290	295	300	
ttc gac agc ctc aga gag aac tcc tac aag acc tct cgc ata gct aca			1203
Phe Asp Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr			
305	310	315	
ttc tgaggcaaac gacagactct taatcagtaa atgttcactg gcattttgaa			1256
Phe			
ggcatggccc aggagaagag acactagcca taaaatctag ttictattta tcaacgigt			1316
gtgaagatgt acctaatgaa gttttgagaa agcacagggt tataggigt taaatttcct			1376
ttagtgaac tcttatttat ttttatgtat tccgtttat ttatttactg ccacgtact			1436
gatattcaga ccttcatgat catccatctg gtgagcagag ctlcatttgt atataacact			1496
ttcagagcct tcccacccat aggtagtict taaaccagggt gaaagagcaa agttcaagt			1556
cctacttaig tgcatttcgc tcatgtaaga gtttttaaga gagggctgat taccacagcc			1616
ctcttttctc ctgaattttt aatgcagaag ttggaatgaa gcaagggaag gcatgtagg			1676
acaggaaagg aaacaatgga aggaaagtga ttcigtgaaa aggacagtga agccagctat			1736
ttlaccceca ggctggattt tttttttttt tttttttttt ttttttttta ccgagtacac			1796
agagiaccce agtgaagaga acgtcatgag tgtaagtgca aatcagtgga aggagcggca			1856
aacigggaca tgcagaattg aatttgctca aaaaaaaaaa aaaaa			1901

<210> 74

<211> 319

<212> PRT

<213> Homo sapiens

<400> 74

Met Met Val Leu Lys Val Glu Glu Leu Val Thr Gly Lys Lys Asn Gly

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Asn Gly Glu Ala Gly Glu Phe Leu Pro Glu Asp Phe Arg Asp Gly Glu			
20	25	30	
Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys Thr Leu			
35	40	45	
Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser Glu Lys			
50	55	60	
Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg Ser Lys			
65	70	75	80
Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys Lys Arg			
85	90	95	
Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro Glu Pro			
100	105	110	
Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys Ala Ala			
115	120	125	
Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp Lys Asn			
130	135	140	
Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His Arg Ala			
145	150	155	160
Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu Ala Gly			
165	170	175	
Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile His Trp			
180	185	190	
Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu Asn Lys			
195	200	205	
Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala Leu His			
210	215	220	

Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu Ile Ala  
 225 230 235 240

Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr Pro Leu  
 245 250 255

His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu Leu Ile  
 260 265 270

Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys Thr Pro  
 275 280 285

Met Asp Leu Val Leu His Trp Gln Asn Gly Thr Lys Ala Ile Phe Asp  
 290 295 300

Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr Phe  
 305 310 315

<210> 75

<211> 5613

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118).. (5475)

<400> 75

cccggagcag ggcgagagct cgcgtcgccg gaaaggaaga cggaagaaa gggcaggcgg 60  
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 atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta gcc ctg tgc aga 165  
 Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg  
 1 5 10 15  
 gcc cga gtg cgc gct cag gaa ccc gag ttc agc tac ggc tgc gca gaa 213



Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu	
20 25 30	
ggc agc tgc tat ccc gcc acg ggc gac ctt ctc atc ggc cga gca cag	261
Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln	
35 40 45	
aag ctt tgc gtg acc tgc acg tgc ggg ctg cac aag ccc gaa ccc tac	309
Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr	
50 55 60	
tgt atc gtc agc cac ttg cag gag gac aaa aaa tgc ttc ata tgc aat	357
Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn	
65 70 75 80	
tcc caa gat cct tat cat gag acc ctg aat cct gac agc cat ctc att	405
Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile	
85 90 95	
gaa aat gtg gtc act aca ttt gct cca aac cgc ctt aag att tgg tgg	453
Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp	
100 105 110	
caa tct gaa aat ggt gtg gaa aat gta act atc caa ctg gat ttg gaa	501
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu	
115 120 125	
gca gaa ttc cat ttt act cat ctc ata atg act ttc aag aca ttc cgt	549
Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg	
130 135 140	
cca gct gct atg ctg ata gaa cga tgc tcc gac ttt ggg aaa acc tgg	597
Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp	
145 150 155 160	

ggt gtg tat aga tac ttc gcc tat gac tgt gag gcc tcg ttt cca ggc	645
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly	
165 170 175	
att tca act ggc ccc atg aaa aaa gtc gat gac ata att tgt gat tct	693
Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser	
180 185 190	
cga tat tct gac att gaa ccc tca act gaa gga gag gtg ata ttt cgt	741
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg	
195 200 205	
gct tta gat cct gct ttc aaa ata gaa gat cct tat agc cca agg ata	789
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile	
210 215 220	
cag aat tta tta aaa att acc aac ttg aga atc aag ttt gtg aaa ctg	837
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu	
225 230 235 240	
cat act ttg gga gat aac ctt ctg gat tcc agg atg gaa atc aga gaa	885
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu	
245 250 255	
aag tat tat tat gca gtt tat gat atg gtg gtt cga gga aat tgc ttc	933
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe	
260 265 270	
tgc tat ggt cat gcc agc gaa tgt gcc cct gtg gat gga ttc aat gaa	981
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu	
275 280 285	
gaa gtg gaa gga atg gtt cac gga cac tgc atg tgc agg cat aac acc	1029
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr	
290 295 300	

aag ggc tta aac tgt gaa ctc tgc atg gat ttc tac cat gat tta cct	1077
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro	
305 310 315 320	
tgg aga cct gct gaa ggc cga aac agc aac gcc tgt aaa aaa tgt aac	1125
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn	
325 330 335	
tgc aat gaa cat tcc atc tct tgt cac ttt gac atg gct gtt tac ctg	1173
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu	
340 345 350	
gcc acg ggg aac gtc agc gga ggc gtg tgt gat gac tgt cag cac aac	1221
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn	
355 360 365	
acc atg ggg cgc aac tgt gag cag tgc aag ccg ttt tac tac cag cac	1269
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His	
370 375 380	
cca gag agg gac atc cga gat cct aat ttc tgt gaa cga tgt acg tgt	1317
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys	
385 390 395 400	
gac cca gct ggc tct caa aat gag gga att tgt gac agc tat act gat	1365
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp	
405 410 415	
ttt tct act ggt ctc att gct ggc cag tgt cgg tgt aaa tta aat gtg	1413
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val	
420 425 430	
gaa gga gaa cat tgt gat gtt tgc aaa gaa ggc ttc tat gat tta agc	1461
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser	

435	440	445	
agt gaa gat cca ttt ggt tgt aaa tct tgt gct tgc aat cct ctg gga	1509		
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly			
450	455	460	
aca att cct gga ggg aat cct tgt gat tcc gag aca ggt cac tgc tac	1557		
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr			
465	470	475	480
tgc aag cgt ctg gtg aca gga cag cat tgt gac cag tgc ctg cca gag	1605		
Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu			
485	490	495	
cac tgg ggc tta agc aat gat ttg gat gga tgt cga cca tgt gac tgt	1653		
His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys			
500	505	510	
gac ctt ggg gga gcc tta aac aac agt tgc ttt gcg gag tca ggc cag	1701		
Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln			
515	520	525	
tgc tca tgc cgg cct cac atg att gga cgt cag tgc aac gaa gtg gaa	1749		
Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu			
530	535	540	
cct ggt tac tac ttt gcc acc ctg gat cac tac ctc tat gaa gcg gag	1797		
Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu			
545	550	555	560
gaa gcc aac ttg ggg cct ggg gtt agc ata gtg gag cgg caa tat atc	1845		
Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile			
565	570	575	
cag gac cgg att ccc tcc tgg act gga gcc ggc ttc gtc cga gtg cct	1893		
Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro			

580	585	590	
gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca tat tcc atg			1941
Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met			
595	600	605	
gag tac gac atc cta att cgc tac gag cca cag cta ccc gac cac tgg			1989
Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp			
610	615	620	
gaa aaa gct gtc atc aca gtg cag cga cct gga agg att cca acc agc			2037
Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser			
625	630	635	640
agc cga tgt ggt aat acc atc ccc gat gat gac aac cag gtg gtg tca			2085
Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser			
645	650	655	
tta tca cca ggc tca aga tat gtc gtc ctt cct cgg ccg gtg tgc ttt			2133
Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe			
660	665	670	
gag aag gga aca aac tac acg gtg agg ttg gag ctg cct cag tac acc			2181
Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr			
675	680	685	
tcc tct gat agc gac gtg gag agc ccc tac acg ctg atc gat tct ctt			2229
Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu			
690	695	700	
gtt ctc atg cca tac tgt aaa tca ctg gac atc ttc acc gtg gga ggt			2277
Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly			
705	710	715	720
tca gga gat ggg gtg gtc acc aac agt gcc tgg gaa acc ttt cag aga			2325

Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg	
725	730
735	
tac cga tgt cta gag aac agc aga agc gtt gtg aaa aca ccg atg aca	2373
Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr	
740	745
750	
gat gtt tgc aga aac atc atc ttt agc att tct gcc ctg tta cac cag	2421
Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln	
755	760
765	
aca ggc ctg gct tgt gaa tgc gac cct cag ggt tgc tta agt tcc gtg	2469
Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val	
770	775
780	
tgt gat ccc aac gga ggc cag tgc cag tgc cgg ccc aac gtg gtt gga	2517
Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly	
785	790
795	800
aga acc tgc aac aga tgt gca cct gga act ttt ggc ttt ggc ccc agt	2565
Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser	
805	810
815	
gga tgc aaa cct tgt gag tgc cat ctg caa gga tct gtc aat gcc ttc	2613
Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe	
820	825
830	
tgc aat ccc gtc act ggc cag tgc cac tgt ttc cag gga gtg tat gct	2661
Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala	
835	840
845	
cgg cag tgt gat cgg tgc tta cct ggg cac tgg ggc ttt cca agt tgc	2709
Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys	
850	855
860	
cag ccc tgc cag tgc aat ggc cac gcc gat gac tgc gac cca gtg act	2757



tgt cag ttc tgc cgg ttt gga tac tat ggt gat gcc ctc cgg cag gac	3189
Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp	
1010	1015
1020	
tgt cga aag tgt gtc tgt aat tac ctg ggc acc gtg caa gag cac tgt	3237
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys	
1025	1030
1035	1040
aac ggc tct gac tgc cag tgc gac aaa gcc act ggt cag tgc ttg tgt	3285
Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys	
1045	1050
1055	
ctt cct aat gtg atc ggg cag aac tgt gac cgc tgt gcg ccc aat acc	3333
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr	
1060	1065
1070	
tgg cag ctg gcc agt ggc act ggc tgt gac cca tgc aac tgc aat gct	3381
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala	
1075	1080
1085	
gct cat tcc ttc ggg cca tct tgc aat gag ttc acg ggg cag tgc cag	3429
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln	
1090	1095
1100	
tgc atg cct ggg ttt gga ggc cgc acc tgc agc gag tgc cag gaa ctc	3477
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu	
1105	1110
1115	1120
ttc tgg gga gac ccc gac gtg gag tgc cga gcc tgt gac tgt gac ccc	3525
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro	
1125	1130
1135	
agg ggc att gag acg cca cag tgt gac cag tcc acg ggc cag tgt gtc	3573
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val	
1140	1145
1150	



tgc gtt gag ggt gtt gag ggt cca cgc tgt gac aag tgc acg cga ggg	3621
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly	
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tac tcg ggg gtc ttc cct gac tgc aca ccc tgc cac cag tgc ttt gct	3669
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala	
1170 1175 1180	
ctc tgg gat gtg atc att gcc gag ctg acc aac agg aca cac aga ttc	3717
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe	
1185 1190 1195 1200	
ctg gag aaa gcc aag gcc ttg aag atc agt ggt gtg atc ggg cct tac	3765
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr	
1205 1210 1215	
cgt gag act gtg gac tcg gtg gag agg aaa gtc agc gag ata aaa gac	3813
Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp	
1220 1225 1230	
atc ctg gcg cag agc ccc gca gca gag cca ctg aaa aac att ggg aat	3861
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn	
1235 1240 1245	
ctc ttt gag gaa gca gag aaa ctg att aaa gat gtt aca gaa atg atg	3909
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met	
1250 1255 1260	
gct caa gta gaa gtg aaa tta tct gac aca act tcc caa agc aac agc	3957
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser	
1265 1270 1275 1280	
aca gcc aaa gaa ctg gat tct cta cag aca gaa gcc gaa agc cta gac	4005
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp	

1285	1290	1295	
aac act gtg aaa gaa ctt gct gaa caa ctg gaa ttt atc aaa aac tca			4053
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser			
1300	1305	1310	
gat att cgg ggt gcc ttg gat agc att acc aag tat ttc cag atg tct			4101
Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser			
1315	1320	1325	
ctt gag gca gag gag agg gtg aat gcc tcc acc aca gaa ccc aac agc			4149
Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser			
1330	1335	1340	
act gtg gag cag tca gcc ctc atg aga gac aga gta gaa gac gtg atg			4197
Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met			
1345	1350	1355	1360
atg gag cga gaa tcc cag ttc aag gaa aaa caa gag gag cag gct cgc			4245
Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg			
1365	1370	1375	
cic ctt gat gaa ctg gca ggc aag cta caa agc cta gac ctt tca gcc			4293
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala			
1380	1385	1390	
gct gcc gaa atg acc tgt gga aca ccc cca ggg gcc tcc tgt tcc gag			4341
Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu			
1395	1400	1405	
act gaa tgt ggc ggg cca aac tgc aga act gac gaa gga gag agg aag			4389
Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys			
1410	1415	1420	
tgt ggg ggg cct ggc tgt ggt ggt ctg gtt act gtt gca cac aac gcc			4437
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala			

1425	1430	1435	1440	
tg	g	caa	atg gac ttg gac	4485
Trp	Gln	Lys	Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala	
	1445	1450	1455	
	gaa	gtg gaa	cag ctc tcc aag atg gtc tct gaa gca aaa ctg agg gca	4533
	Glu	Val	Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala	
	1460	1465	1470	
	gat	gag gca	aaa caa agt gct gaa gac att ctg ttg aag aca aat gct	4581
	Asp	Glu	Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala	
	1475	1480	1485	
	acc	aaa gaa	aaa atg gac aag agc aat gag gag ctg aga aat cta atc	4629
	Thr	Lys	Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile	
	1490	1495	1500	
	aag	caa atc	aga aac ttt ttg acc cag gat agt gct gat ttg gac agc	4677
	Lys	Gln	Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser	
1505	1510	1515	1520	
	att	gaa gca	gtt gct aat gaa gta ttg aaa atg gag atg cct agc acc	4725
	Ile	Glu	Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr	
	1525	1530	1535	
	cca	cag cag	tta cag aac ttg aca gaa gat ata cgt gaa cga gtt gaa	4773
	Pro	Gln	Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu	
	1540	1545	1550	
	agc	ctt tct	caa gta gag gtt att ctt cag cat agt gct gct gac att	4821
	Ser	Leu	Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile	
	1555	1560	1565	
	gcc	aga gct	gag atg ttg tta gaa gaa gct aaa aga gca agc aaa agt	4869

Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser			
1570	1575	1580	
gca aca gat gtt aaa gtc act gca gat atg gta aag gaa gct ctg gaa			4917
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu			
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gaa gca gaa aag gcc cag gtc gca gca gag aag gca att aaa caa gca			4965
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala			
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gat gaa gac att caa gga acc cag aac ctg tta act tcg att gag tct			5013
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser			
1620	1625	1630	
gaa aca gca gct tct gag gaa acc ttg ttc aac gcg tcc cag cgc atc			5061
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile			
1635	1640	1645	
agc gag tta gag agg aat gtg gaa gaa ctt aag cgg aaa gct gcc caa			5109
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln			
1650	1655	1660	
aac tcc ggg gag gca gaa tat att gaa aaa gta gta tat act gtg aag			5157
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys			
1665	1670	1675	1680
caa agt gca gaa gat gtt aag aag act tta gat ggt gaa ctt gat gaa			5205
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu			
1685	1690	1695	
aag tat aaa aaa gta gaa aat tta att gcc aaa aaa act gaa gag tca			5253
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser			
1700	1705	1710	
gct gat gcc aga agg aaa gcc gaa atg cta caa aat gaa gca aaa act			5301

Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr

1715

1720

1725

ctt tta gct caa gca aat agc aag ctg caa ctg ctc aaa gat tta gaa 5349

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu

1730

1735

1740

aga aaa tat gaa gac aat caa aga tac tta gaa gat aaa gct caa gaa 5397

Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu

1745

1750

1755

1760

tta gca aga ctg gaa gga gaa gtc cgt tca ctc cta aag gat ata agc 5445

Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser

1765

1770

1775

cag aaa gtt gct gtg tat agc aca tgc ttg taacagagga gaataaaaaa 5495

Gln Lys Val Ala Val Tyr Ser Thr Cys Leu

1780

1785

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ataaaacatc acctatttta tgtttttaat cacattttgt atgagttaaa taaagccc 5613

<210> 76

<211> 1786

<212> PRT

<213> Homo sapiens

<400> 76

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1

5

10

15

Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu

20

25

30

Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln

35	40	45	
Lys	Leu	Ser	Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
50	55	60	
Cys	Ile	Val	Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
65	70	75	80
Ser	Gln	Asp	Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
85	90	95	
Glu	Asn	Val	Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
100	105	110	
Gln	Ser	Glu	Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
115	120	125	
Ala	Glu	Phe	His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
130	135	140	
Pro	Ala	Ala	Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145	150	155	160
Gly	Val	Tyr	Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
165	170	175	
Ile	Ser	Thr	Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
180	185	190	
Arg	Tyr	Ser	Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
195	200	205	
Ala	Leu	Asp	Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
210	215	220	
Gln	Asn	Leu	Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225	230	235	240
His	Thr	Leu	Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu

245	250	255
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe		
260	265	270
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu		
275	280	285
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr		
290	295	300
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro		
305	310	315
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn		
325	330	335
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu		
340	345	350
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn		
355	360	365
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His		
370	375	380
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys		
385	390	395
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp		
405	410	415
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val		
420	425	430
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser		
435	440	445
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly		
450	455	460

Thr	Ile	Pro	Gly	Gly	Asn	Pro	Cys	Asp	Ser	Glu	Thr	Gly	His	Cys	Tyr
465					470					475					480
Cys	Lys	Arg	Leu	Val	Thr	Gly	Gln	His	Cys	Asp	Gln	Cys	Leu	Pro	Glu
				485						490					495
His	Trp	Gly	Leu	Ser	Asn	Asp	Leu	Asp	Gly	Cys	Arg	Pro	Cys	Asp	Cys
				500						505					510
Asp	Leu	Gly	Gly	Ala	Leu	Asn	Asn	Ser	Cys	Phe	Ala	Glu	Ser	Gly	Gln
				515						520					525
Cys	Ser	Cys	Arg	Pro	His	Met	Ile	Gly	Arg	Gln	Cys	Asn	Glu	Val	Glu
				530						535					540
Pro	Gly	Tyr	Tyr	Phe	Ala	Thr	Leu	Asp	His	Tyr	Leu	Tyr	Glu	Ala	Glu
545					550					555					560
Glu	Ala	Asn	Leu	Gly	Pro	Gly	Val	Ser	Ile	Val	Glu	Arg	Gln	Tyr	Ile
				565						570					575
Gln	Asp	Arg	Ile	Pro	Ser	Trp	Thr	Gly	Ala	Gly	Phe	Val	Arg	Val	Pro
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Glu	Gly	Ala	Tyr	Leu	Glu	Phe	Phe	Ile	Asp	Asn	Ile	Pro	Tyr	Ser	Met
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Glu	Tyr	Asp	Ile	Leu	Ile	Arg	Tyr	Glu	Pro	Gln	Leu	Pro	Asp	His	Trp
				610						615					620
Glu	Lys	Ala	Val	Ile	Thr	Val	Gln	Arg	Pro	Gly	Arg	Ile	Pro	Thr	Ser
625					630					635					640
Ser	Arg	Cys	Gly	Asn	Thr	Ile	Pro	Asp	Asp	Asp	Asn	Gln	Val	Val	Ser
				645						650					655
Leu	Ser	Pro	Gly	Ser	Arg	Tyr	Val	Val	Leu	Pro	Arg	Pro	Val	Cys	Phe
				660						665					670



Glu	Lys	Gly	Thr	Asn	Tyr	Thr	Val	Arg	Leu	Glu	Leu	Pro	Gln	Tyr	Thr
675				680				685							
Ser	Ser	Asp	Ser	Asp	Val	Glu	Ser	Pro	Tyr	Thr	Leu	Ile	Asp	Ser	Leu
690				695				700							
Val	Leu	Met	Pro	Tyr	Cys	Lys	Ser	Leu	Asp	Ile	Phe	Thr	Val	Gly	Gly
705				710				715				720			
Ser	Gly	Asp	Gly	Val	Val	Thr	Asn	Ser	Ala	Trp	Glu	Thr	Phe	Gln	Arg
725				730				735							
Tyr	Arg	Cys	Leu	Glu	Asn	Ser	Arg	Ser	Val	Val	Lys	Thr	Pro	Met	Thr
740				745				750							
Asp	Val	Cys	Arg	Asn	Ile	Ile	Phe	Ser	Ile	Ser	Ala	Leu	Leu	His	Gln
755				760				765							
Thr	Gly	Leu	Ala	Cys	Glu	Cys	Asp	Pro	Gln	Gly	Ser	Leu	Ser	Ser	Val
770				775				780							
Cys	Asp	Pro	Asn	Gly	Gly	Gln	Cys	Gln	Cys	Arg	Pro	Asn	Val	Val	Gly
785				790				795				800			
Arg	Thr	Cys	Asn	Arg	Cys	Ala	Pro	Gly	Thr	Phe	Gly	Phe	Gly	Pro	Ser
805				810				815							
Gly	Cys	Lys	Pro	Cys	Glu	Cys	His	Leu	Gln	Gly	Ser	Val	Asn	Ala	Phe
820				825				830							
Cys	Asn	Pro	Val	Thr	Gly	Gln	Cys	His	Cys	Phe	Gln	Gly	Val	Tyr	Ala
835				840				845							
Arg	Gln	Cys	Asp	Arg	Cys	Leu	Pro	Gly	His	Trp	Gly	Phe	Pro	Ser	Cys
850				855				860							
Gln	Pro	Cys	Gln	Cys	Asn	Gly	His	Ala	Asp	Asp	Cys	Asp	Pro	Val	Thr
865				870				875				880			
Gly	Glu	Cys	Leu	Asn	Cys	Gln	Asp	Tyr	Thr	Met	Gly	His	Asn	Cys	Glu

885	890	895
Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp		
900	905	910
His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln		
915	920	925
Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys		
930	935	940
Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser		
945	950	955
Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys		
965	970	975
Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys		
980	985	990
Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His		
995	1000	1005
Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp		
1010	1015	1020
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys		
1025	1030	1035
Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys		
1045	1050	1055
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr		
1060	1065	1070
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala		
1075	1080	1085
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln		

1090	1095	1100	
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu			
1105	1110	1115	1120
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro			
	1125	1130	1135
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val			
	1140	1145	1150
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly			
	1155	1160	1165
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala			
	1170	1175	1180
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe			
1185	1190	1195	1200
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr			
	1205	1210	1215
Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp			
	1220	1225	1230
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn			
	1235	1240	1245
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met			
	1250	1255	1260
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser			
1265	1270	1275	1280
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp			
	1285	1290	1295
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser			
	1300	1305	1310

Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser			
1315	1320	1325	
Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser			
1330	1335	1340	
Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met			
1345	1350	1355	1360
Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg			
1365	1370	1375	
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala			
1380	1385	1390	
Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu			
1395	1400	1405	
Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys			
1410	1415	1420	
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala			
1425	1430	1435	1440
Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala			
1445	1450	1455	
Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala			
1460	1465	1470	
Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala			
1475	1480	1485	
Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile			
1490	1495	1500	
Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser			
1505	1510	1515	1520

Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr			
1525	1530	1535	
Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu			
1540	1545	1550	
Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile			
1555	1560	1565	
Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser			
1570	1575	1580	
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu			
1585	1590	1595	1600
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala			
1605	1610	1615	
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser			
1620	1625	1630	
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile			
1635	1640	1645	
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln			
1650	1655	1660	
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys			
1665	1670	1675	1680
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu			
1685	1690	1695	
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser			
1700	1705	1710	
Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr			
1715	1720	1725	
Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu			

1730	1735	1740	
Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu			
1745	1750	1755	1760
Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser			
	1765	1770	1775
Gln Lys Val Ala Val Tyr Ser Thr Cys Leu			
1780	1785		

<210> 77  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (27).. (335)  
 <400> 77

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                                Met Lys Ser Leu Ile Leu Leu Ala Ile
                                1             5

ctg gcc gcc tta gcg gta gta act ttg tgt tat gaa tca cat gaa agc  101
Leu Ala Ala Leu Ala Val Val Thr Leu Cys Tyr Glu Ser His Glu Ser

  10             15             20             25
atg gaa tct tat gaa ctt aat ccc ttc att aac agg aga aat gca aat  149
Met Glu Ser Tyr Glu Leu Asn Pro Phe Ile Asn Arg Arg Asn Ala Asn

          30             35             40
acc ttc ata tcc cct cag cag aga tgg aga gct aaa gtc caa gag agg  197
Thr Phe Ile Ser Pro Gln Gln Arg Trp Arg Ala Lys Val Gln Glu Arg

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45	50	55	
atc cga gaa cgc tct aag cct gtc cac gag ctc aat agg gaa gcc tgt			245
Ile Arg Glu Arg Ser Lys Pro Val His Glu Leu Asn Arg Glu Ala Cys			
60	65	70	
gat gac tac aga ctt tgc gaa cgc tac gcc atg gtt tat gga tac aat			293
Asp Asp Tyr Arg Leu Cys Glu Arg Tyr Ala Met Val Tyr Gly Tyr Asn			
75	80	85	
gct gcc tat aat cgc tac ttc agg aag cgc cga ggg acc aaa			335
Ala Ala Tyr Asn Arg Tyr Phe Arg Lys Arg Arg Gly Thr Lys			
90	95	100	
tgagactgag ggaagaaaaa aaatctcttt tttctggag gctggcacct gatcttgiat			395
ccccctgtag cagcattact gaaatacata ggcttatata caatgcttct ticcgtata			455
ttctcttgtc tggctgcacc cttttttccc gccccagat tgataagtaa tgaaagtgca			515
ctgcagtgag ggtcaaagga gagtcaacat atgtgattgt tccataataa acttctgggtg			575
tgatactttc			585

<210> 78

<211> 103

<212> PRT

<213> Homo sapiens

<400> 78

Met Lys Ser Leu Ile Leu Leu Ala Ile Leu Ala Ala Leu Ala Val Val

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Thr Leu Cys Tyr Glu Ser His Glu Ser Met Glu Ser Tyr Glu Leu Asn			

20	25	30
Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln		

35	40	45
----	----	----

Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro

50

55

60

Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu

65

70

75

80

Arg Tyr Ala Met Val Tyr Gly Tyr Asn Ala Ala Tyr Asn Arg Tyr Phe

85

90

95

Arg Lys Arg Arg Gly Thr Lys

100

<210> 79

<211> 1775

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6).. (1148)

<400> 79

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Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val

1

5

10

15

ttg gcc gag aac tcg gat gat tat gat ctc atg tat gtg aat ttg gac 98

Leu Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp

20

25

30

aac gaa ata gac aat gga ctc cat ccc act gag gac ccc acg ccg tgc 146

Asn Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys

35

40

45

gcc tgc ggt cag gag cac tcg gaa tgg gac aag ctc ttc atc atg ctg 194



Ala Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu	
50 55 60	
gag aac tcg cag atg aga gag cgc atg ctg ctg caa gcc acg gac gac	242
Glu Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp	
65 70 75	
gtc ctg cgg ggc gag ctg cag agg ctg cgg gag gag ctg ggc cgg ctc	290
Val Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu	
80 85 90 95	
gcg gaa agc ctg gcg agg ccg tgc gcg ccg ggg gct ccc gca gag gcc	338
Ala Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala	
100 105 110	
agg ctg acc agt gct ctg gac gag ctg ctg cag gcg acc cgc gac gcg	386
Arg Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala	
115 120 125	
ggc cgc agg ctg gcg cgt atg gag ggc gcg gag gcg cag cgc cca gag	434
Gly Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu	
130 135 140	
gag gcg ggg cgc gcc ctg gcc gcg gtg cta gag gag ctg cgg cag acg	482
Glu Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr	
145 150 155	
cga gcc gac ctg cac gcg gtg cag ggc tgg gct gcc cgg agc tgg ctg	530
Arg Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu	
160 165 170 175	
ccg gca ggt tgt gaa aca gct att tta ttc cca atg cgt tcc aag aag	578
Pro Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys	
180 185 190	

att ttt gga agc gtg cat cca gig aga cca atg agg ctt gag tct ttt	626
Ile Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe	
195 200 205	
agt gcc tgc att tgg gtc aaa gcc aca gat gta tta aac aaa acc atc	674
Ser Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile	
210 215 220	
ctg ttt tcc tat ggc aca aag agg aat cca tat gaa atc cag ctg tat	722
Leu Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr	
225 230 235	
ctc agc tac caa tcc ata gtg ttt gtg gtg ggt gga gag gag aac aaa	770
Leu Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys	
240 245 250 255	
ctg gtt gct gaa gcc atg gtt tcc ctg gga agg tgg acc cac ctg tgc	818
Leu Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys	
260 265 270	
ggc acc tgg aat tca gag gaa ggg ctc aca tcc ttg tgg gta aat ggt	866
Gly Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly	
275 280 285	
gaa ctg gcg gct acc act gtt gag atg gcc aca ggt cac att gtt cct	914
Glu Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro	
290 295 300	
gag gga gga atc ctg cag att ggc caa gaa aag aat ggc tgc tgt gtg	962
Glu Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val	
305 310 315	
ggt ggt ggc ttt gat gaa aca tta gcc ttc tct ggg aga ctc aca ggc	1010
Gly Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly	
320 325 330 335	

ttc aat atc tgg gat agt gtt ctt agc aat gaa gag ata aga gag acc 1058

Phe Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr

340

345

350

gga gga gca gag tct tgt cac atc cgg ggg aat att gtt ggg tgg gga 1106

Gly Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly

355

360

365

gtc aca gag atc cag cca cat gga gga gct cag tat gtt tca 1148

Val Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser

370

375

380

taaatgttgt gaaactccac ttgaagccaa agaaagaaac tcacacttaa aacacatgcc 1208

agttgggaag gtcigaaaac tcagtgcata ataggaacac ttgagactaa tgaaagagag 1268

agttgagacc aatctttatt tgtactggcc aaatactgaa taaacagtig aaggaaagac 1328

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tagtttatgt gttataatcg aatgtcacgt ttttgagaag atagtcatat aagttatatt 1688

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<210> 80

<211> 381

<212> PRT

<213> Homo sapiens

<400> 80

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val Leu

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	20		25		30										
Glu	Ile	Asp	Asn	Gly	Leu	His	Pro	Thr	Glu	Asp	Pro	Thr	Pro	Cys	Ala
	35		40		45										
Cys	Gly	Gln	Glu	His	Ser	Glu	Trp	Asp	Lys	Leu	Phe	Ile	Met	Leu	Glu
	50		55		60										
Asn	Ser	Gln	Met	Arg	Glu	Arg	Met	Leu	Leu	Gln	Ala	Thr	Asp	Asp	Val
	65		70		75										
Leu	Arg	Gly	Glu	Leu	Gln	Arg	Leu	Arg	Glu	Glu	Leu	Gly	Arg	Leu	Ala
	85		90		95										
Glu	Ser	Leu	Ala	Arg	Pro	Cys	Ala	Pro	Gly	Ala	Pro	Ala	Glu	Ala	Arg
	100		105		110										
Leu	Thr	Ser	Ala	Leu	Asp	Glu	Leu	Leu	Gln	Ala	Thr	Arg	Asp	Ala	Gly
	115		120		125										
Arg	Arg	Leu	Ala	Arg	Met	Glu	Gly	Ala	Glu	Ala	Gln	Arg	Pro	Glu	Glu
	130		135		140										
Ala	Gly	Arg	Ala	Leu	Ala	Ala	Val	Leu	Glu	Glu	Leu	Arg	Gln	Thr	Arg
	145		150		155										
Ala	Asp	Leu	His	Ala	Val	Gln	Gly	Trp	Ala	Ala	Arg	Ser	Trp	Leu	Pro
	165		170		175										
Ala	Gly	Cys	Glu	Thr	Ala	Ile	Leu	Phe	Pro	Met	Arg	Ser	Lys	Lys	Ile
	180		185		190										
Phe	Gly	Ser	Val	His	Pro	Val	Arg	Pro	Met	Arg	Leu	Glu	Ser	Phe	Ser
	195		200		205										
Ala	Cys	Ile	Trp	Val	Lys	Ala	Thr	Asp	Val	Leu	Asn	Lys	Thr	Ile	Leu

210	215	220	
Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr Leu			
225	230	235	240
Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys Leu			
245	250	255	
Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys Gly			
260	265	270	
Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly Glu			
275	280	285	
Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro Glu			
290	295	300	
Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val Gly			
305	310	315	320
Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly Phe			
325	330	335	
Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr Gly			
340	345	350	
Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly Val			
355	360	365	
Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser			
370	375	380	

<210> 81

<211> 2312

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (146).. (1192)

<400> 81

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ctccgctccg cccgcagtcg caacc atg acc gcc gcc agt atg ggc ccc gtc 172

Met Thr Ala Ala Ser Met Gly Pro Val

1

5

cgc gtc gcc ttc gtg gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc 220

Arg Val Ala Phe Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val

10

15

20

25

ggc cag aac tgc agc ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg 268

Gly Gln Asn Cys Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro

30

35

40

cgc tgc ccg gcg ggc gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc 316

Arg Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys

45

50

55

cgc gtc tgc gcc aag cag ctg ggc gag ctg tgc acc gag cgc gac ccc 364

Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro

60

65

70

tgc gac ccg cac aag ggc ctc ttc tgc gac ttc ggc tcc ccg gcc aac 412

Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn

75

80

85

cgc aag atc ggc gtg tgc acc gcc aaa gat ggt gct ccc tgc atc ttc 460

Arg Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe

90

95

100

105

ggt ggt acg gtg tac cgc agc gga gag tcc ttc cag agc agc tgc aag 508

Gly Gly Thr Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys	
110	115
120	
tac cag tgc acg tgc ctg gac ggg gcg gtc ggc tgc atg ccc ctg tgc	556
Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys	
125	130
135	
agc atg gac gtt cgt ctg ccc agc cct gac tgc ccc ttc ccg agg agg	604
Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg	
140	145
150	
gtc aag ctg ccc ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc	652
Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro	
155	160
165	
aag gac caa acc gtg gtt ggg cct gcc ctg gcg gct tac cga ctg gaa	700
Lys Asp Gln Thr Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu	
170	175
180	185
gac acg ttt ggc cca gac cca act atg att aga gcc aac tgc ctg gtc	748
Asp Thr Phe Gly Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val	
190	195
200	
cag acc aca gag tgg agc gcc tgt tcc aag acc tgt ggg atg ggc atc	796
Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile	
205	210
215	
tcc acc cgg gtt acc aat gac aac gcc tcc tgc agg cta gag aag cag	844
Ser Thr Arg Val Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln	
220	225
230	
agc cgc ctg tgc atg gtc agg cct tgc gaa gct gac ctg gaa gag aac	892
Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn	
235	240
245	

att aag aag ggc aaa aag tgc atc cgt act ccc aaa atc tcc aag cct 940  
 Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro  
 250 255 260 265  
 atc aag ttt gag ctt tct ggc tgc acc agc atg aag aca tac cga gct 988  
 Ile Lys Phe Glu Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala  
 270 275 280  
 aaa ttc tgt gga gta tgt acc gac ggc cga tgc tgc acc ccc cac aga 1036  
 Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg  
 285 290 295  
 acc acc acc ctg ccg gtg gag ttc aag tgc cct gac ggc gag gtc atg 1084  
 Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met  
 300 305 310  
 aag aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt 1132  
 Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys  
 315 320 325  
 ccc gga gac aat gac atc ttt gaa tcg ctg tac tac agg aag atg tac 1180  
 Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr  
 330 335 340 345  
 gga gac atg gca tgaagccaga gaggagaga cattaactca ttagactgga 1232  
 Gly Asp Met Ala  
 actigaactg attcacatct catctttccg taaaaatgat ttcagtagca caagttatct 1292  
 aaatctgttt ttctaactgg gggaaaagat tcccaccaa ttcaaacat tgtgccatgt 1352  
 caaacaaata gtctatcttc ccagacact gggttgaaga atgttaagac ttgacagtgg 1412  
 aactacatta gtacacagca ccagaatgta tattaagggtg tggctttagg agcagtggga 1472  
 ggglaccagc agaaaggtaa giatcatcag atagctctta tacgagtaat atgcctgcta 1532  
 ttgaagtgt aatigagaag gaaaatttta gcgtgctcac tgacctgcct gtagccccag 1592  
 tgacagctag gatgtgcatt ctccagccat caagagactg agtcaagttg ttccttaagt 1652



cagaacagca gactcagctc tgacattcig attcgaatga cactgttcag gaatcggaat 1712  
cctgtcgaat agactggaca gcitgtggca agtgaatttc ctgtaacaag ccagattttt 1772  
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gataattcaa tgitagcctc aatttctgaa caccaataggt agaattgaaa gcttgtctga 1952  
tcgttcaaag catgaaaatgg atacttataat ggaaattctc tcagatagaa tgacagtccg 2012  
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tgactctata tagcigaica gttttttcac ctggaagcat ttgtttctac ttgataatga 2192  
ctgtttttcg gacagtttat ttgttgagag tgtgacaaa agttacaatg ttgcaccttt 2252  
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<210> 82

<211> 349

<212> PRT

<213> Homo sapiens

<400> 82

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1 5 10 15

Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro

20 25 30

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser

35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu

50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu

65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr			
	85	90	95
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser			
	100	105	110
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp			
	115	120	125
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro			
	130	135	140
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys			
145	150	155	160
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly			
	165	170	175
Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro			
	180	185	190
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala			
	195	200	205
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp			
	210	215	220
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg			
225	230	235	240
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys			
	245	250	255
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly			
	260	265	270
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr			
	275	280	285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu  
 290 295 300  
 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile  
 305 310 315 320  
 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe  
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 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
 340 345

<210> 83  
 <211> 2954  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (173).. (1525)  
 <400> 83

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 taaccgggtc aatgtgtgga atatggggg gctcggctgc agacttggcc aa atg gac 178

Met Asp

1

ggg act att aag gag gct ctg tcg gtg gtg agc gac gac cag tcc ctc 226  
 Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln Ser Leu  
 5 10 15  
 ttt gac tca gcg tac gga gcg gca gcc cat ctc ccc aag gcc gac atg 274  
 Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala Asp Met

20	25	30	
act gcc tgc ggg agt cct gac tac ggg cag ccc cac aag atc aac ccc	322		
Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile Asn Pro			
35	40	45	50
ctc cca cca cag cag gag tgg atc aat cag cca gig agg gtc aac gtc	370		
Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val Asn Val			
55	60	65	
aag cgg gag tat gac cac atg aat gga tcc agg gag tct ccg gtg gac	418		
Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro Val Asp			
70	75	80	
tgc agc gtt agc aaa tgc agc aag ctg gtg ggc gga ggc gag tcc aac	466		
Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu Ser Asn			
85	90	95	
ccc atg aac tac aac agc tat atg gac gag aag aat ggc ccc cct cct	514		
Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro Pro Pro			
100	105	110	
ccc aac atg acc acc aac gag agg aga gtc atc gtc ccc gca gac ccc	562		
Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala Asp Pro			
115	120	125	130
aca ctg tgg aca cag gag cat gtg agg caa tgg ctg gag tgg gcc ata	610		
Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp Ala Ile			
135	140	145	
aag gag tac agc ttg atg gag atc gac aca tcc ttt ttc cag aac atg	658		
Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln Asn Met			
150	155	160	
gat ggc aag gaa ctg tgt aaa atg aac aag gag gac ttc ctc cgc gcc	706		
Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu Arg Ala			

165	170	175	
acc acc ctc tac aac acg gaa gtg ctg ttg tca cac ctc agt tac ctc	754		
Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser Tyr Leu			
180	185	190	
agg gaa agt tca ctg ctg gcc tat aat aca acc tcc cac acc gac caa	802		
Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr Asp Gln			
195	200	205	210
tcc tca cga ttg agt gtc aaa gaa gac cct tct tat gac tca gtc aga	850		
Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser Val Arg			
215	220	225	
aga gga gct tgg ggc aat aac atg aat tct ggc ctc aac aaa agt cct	898		
Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys Ser Pro			
230	235	240	
ccc ctt gga ggg gca caa acg atc agt aag aat aca gag caa cgg ccc	946		
Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln Arg Pro			
245	250	255	
cag cca gat ccg tat cag atc ctg ggc ccg acc agc agt cgc cta gcc	994		
Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala			
260	265	270	
aac cct gga agc ggg cag atc cag ctg tgg caa ttc ctc ctg gag ctg	1042		
Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu			
275	280	285	290
ctc tcc gac agc gcc aac gcc agc tgt atc acc tgg gag ggg acc aac	1090		
Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly Thr Asn			
295	300	305	
ggg gag ttc aaa atg acg gac ccc gat gag gtg gcc agg cgc tgg ggc	1138		

Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly	
310	315
320	
gag cgg aaa agc aag ccc aac atg aat tac gac aag ctg agc cgg gcc	1186
Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala	
325	330
335	
ctc cgt tat tac tat gat aaa aac att atg acc aaa gtg cac ggc aaa	1234
Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His Gly Lys	
340	345
350	
aga tat gct tac aaa ttt gac ttc cac ggc att gcc cag gct ctg cag	1282
Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala Leu Gln	
355	360
365	370
cca cat ccg acc gag tcg tcc atg tac aag tac cct tct gac atc tcc	1330
Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp Ile Ser	
375	380
385	
tac atg cct tcc caa cat gcc cac cag cag aag gtg aac ttt gtc cct	1378
Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe Val Pro	
390	395
400	
ccc cat cca tcc tcc atg cct gtc act tcc tcc agc ttc ttt gga gcc	1426
Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe Gly Ala	
405	410
415	
gca tca caa tac tgg acc tcc acg ggg gga atc tac ccc aac ccc aac	1474
Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn Pro Asn	
420	425
430	
gtc ccc cgc cat cct aac acc cac gtg cct tca cac tta ggc agc tac	1522
Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly Ser Tyr	
435	440
445	450
tac tagaagctta ctcatcagtg gccttctagc tgaagcccat ccigcacact	1575

Tyr

tactggatgc ttiggactca acaggacata tgtggccttg aagggaagac aaaactggat 1635  
gttctttctt gttggataga accttigtat ttgttcttta aaaataatit ttttaatggt 1695  
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atatatataa ttttgcaggt aattgttgac ttttttaact atattaagt ttaagctgac 2895  
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<210> 84

<211> 451

<212> PRT

<213> Homo sapiens

<400> 84

Met	Asp	Gly	Thr	Ile	Lys	Glu	Ala	Leu	Ser	Val	Val	Ser	Asp	Asp	Gln
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Ser	Leu	Phe	Asp	Ser	Ala	Tyr	Gly	Ala	Ala	Ala	His	Leu	Pro	Lys	Ala
			20					25					30		
Asp	Met	Thr	Ala	Ser	Gly	Ser	Pro	Asp	Tyr	Gly	Gln	Pro	His	Lys	Ile
			35					40					45		
Asn	Pro	Leu	Pro	Pro	Gln	Gln	Glu	Trp	Ile	Asn	Gln	Pro	Val	Arg	Val
			50					55					60		
Asn	Val	Lys	Arg	Glu	Tyr	Asp	His	Met	Asn	Gly	Ser	Arg	Glu	Ser	Pro
			65					70					75		80
Val	Asp	Cys	Ser	Val	Ser	Lys	Cys	Ser	Lys	Leu	Val	Gly	Gly	Gly	Glu
				85						90					95
Ser	Asn	Pro	Met	Asn	Tyr	Asn	Ser	Tyr	Met	Asp	Glu	Lys	Asn	Gly	Pro
			100							105					110
Pro	Pro	Pro	Asn	Met	Thr	Thr	Asn	Glu	Arg	Arg	Val	Ile	Val	Pro	Ala
			115							120					125
Asp	Pro	Thr	Leu	Trp	Thr	Gln	Glu	His	Val	Arg	Gln	Trp	Leu	Glu	Trp
			130							135					140
Ala	Ile	Lys	Glu	Tyr	Ser	Leu	Met	Glu	Ile	Asp	Thr	Ser	Phe	Phe	Gln
			145							150					155
Asn	Met	Asp	Gly	Lys	Glu	Leu	Cys	Lys	Met	Asn	Lys	Glu	Asp	Phe	Leu
				165						170					175
Arg	Ala	Thr	Thr	Leu	Tyr	Asn	Thr	Glu	Val	Leu	Leu	Ser	His	Leu	Ser



	180	185	190
Tyr	Leu	Arg	Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr
	195	200	205
Asp	Gln Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser		
	210	215	220
Val	Arg Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys		
225	230	235	240
Ser	Pro Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln		
	245	250	255
Arg	Pro Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg		
	260	265	270
Leu	Ala Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu		
	275	280	285
Glu	Leu Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly		
	290	295	300
Thr	Asn Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg		
305	310	315	320
Trp	Gly Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser		
	325	330	335
Arg	Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His		
	340	345	350
Gly	Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala		
	355	360	365
Leu	Gln Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp		
	370	375	380
Ile	Ser Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe		
385	390	395	400

Val Pro Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe

405

410

415

Gly Ala Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn

420

425

430

Pro Asn Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly

435

440

445

Ser Tyr Tyr

450

<210> 85

<211> 1817

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (361)

<400> 85

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1

5

10

15

agg cct gca ggg gat gga acc ttc cag aag tgg gca gct gtg gtg gtg 97

Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val

20

25

30

cct tct gga gag gag cag aga tac acg tgc cat gtg cag cat gag ggg 145

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

35

40

45

cta ccc gag ccc gtc acc ctg aga tgg aag ccg gct tcc cag ccc acc 193

Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr  
 50 55 60  
 atc ccc atc gtg ggc atc att gct ggc ctg gtt ctc ctt gga tct gtg 241  
 Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val  
 65 70 75 80  
 gtc tct gga gct gtg gtt gct gct gtg ata tgg agg aag aag agc tca 289  
 Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser  
 85 90 95  
 ggt gga aaa gga ggg agc tac tct aag gct gag tgg agc gac agt gcc 337  
 Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala  
 100 105 110  
 cag ggg tct gag tct cac agc ttg taaagcctga gacagctgcc ttgtgtgcga 391  
 Gln Gly Ser Glu Ser His Ser Leu  
 115 120  
 ctgagatgca cagctgcctt gtgtgcgact gagatgcagg atttcctcac gcctccccta 451  
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<210> 86

<211> 120

<212> PRT

<213> Homo sapiens

<400> 86

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Arg	Pro	Ala	Gly	Asp	Gly	Thr	Phe	Gln	Lys	Trp	Ala	Ala	Val	Val	Val
				20				25				30			
Pro	Ser	Gly	Glu	Glu	Gln	Arg	Tyr	Thr	Cys	His	Val	Gln	His	Glu	Gly
				35				40				45			
Leu	Pro	Glu	Pro	Val	Thr	Leu	Arg	Trp	Lys	Pro	Ala	Ser	Gln	Pro	Thr
				50				55				60			
Ile	Pro	Ile	Val	Gly	Ile	Ile	Ala	Gly	Leu	Val	Leu	Leu	Gly	Ser	Val

65	70	75	80
Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser			
	85	90	95
Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala			
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Gln Gly Ser Glu Ser His Ser Leu			
	115	120	

<210> 87

<211> 2876

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1281)

<400> 87

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      Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu
      1           5           10
ggc ctg gcc ctt gtc ttt ggt gaa ggg tct gct gtg cac cat ccc cca 159
Gly Leu Ala Leu Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro
      15           20           25
tcc tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag 207
Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln
      30           35           40
cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat 255

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Val	Asn	Ala	Leu	Tyr	Phe	Asn	Gly	Gln	Trp	Lys	Thr	Pro	Phe	Pro	Asp		
190						195						200					
tcc	agc	acc	cac	cgc	cgc	ctc	ttc	cac	aaa	tca	gac	ggc	agc	act	gtc	735	
Ser	Ser	Thr	His	Arg	Arg	Leu	Phe	His	Lys	Ser	Asp	Gly	Ser	Thr	Val		
205					210					215					220		
tct	gig	ccc	atg	atg	gct	cag	acc	aac	aag	ttc	aac	tat	act	gag	ttc	783	
Ser	Val	Pro	Met	Met	Ala	Gln	Thr	Asn	Lys	Phe	Asn	Tyr	Thr	Glu	Phe		
				225					230					235			
acc	acg	ccc	gat	ggc	cat	tac	tac	gac	atc	ctg	gaa	ctg	ccc	tac	cac	831	
Thr	Thr	Pro	Asp	Gly	His	Tyr	Tyr	Asp	Ile	Leu	Glu	Leu	Pro	Tyr	His		
				240				245					250				
ggg	gac	acc	ctc	agc	atg	ttc	att	gct	gcc	cct	tat	gaa	aaa	gag	gtg	879	
Gly	Asp	Thr	Leu	Ser	Met	Phe	Ile	Ala	Ala	Pro	Tyr	Glu	Lys	Glu	Val		
				255				260					265				
cct	ctc	tct	gcc	ctc	acc	aac	att	ctg	agt	gcc	cag	ctc	atc	agc	cac	927	
Pro	Leu	Ser	Ala	Leu	Thr	Asn	Ile	Leu	Ser	Ala	Gln	Leu	Ile	Ser	His		
270						275						280					
tgg	aaa	ggc	aac	atg	acc	agg	ctg	ccc	cgc	ctc	ctg	gtt	ctg	ccc	aag	975	
Trp	Lys	Gly	Asn	Met	Thr	Arg	Leu	Pro	Arg	Leu	Leu	Val	Leu	Pro	Lys		
285						290					295				300		
ttc	tcc	ctg	gag	act	gaa	gtc	gac	ctc	agg	aag	ccc	cta	gag	aac	ctg	1023	
Phe	Ser	Leu	Glu	Thr	Glu	Val	Asp	Leu	Arg	Lys	Pro	Leu	Glu	Asn	Leu		
				305						310				315			
gga	atg	acc	gac	atg	ttc	aga	cag	ttt	cag	gct	gac	ttc	acg	agt	ctt	1071	
Gly	Met	Thr	Asp	Met	Phe	Arg	Gln	Phe	Gln	Ala	Asp	Phe	Thr	Ser	Leu		
				320					325				330				

tca gac caa gag cct ctc cac gtc gcg cag gcg ctg cag aaa gtg aag 1119

Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys

335

340

345

atc gag gtg aac gag agt ggc acg gtg gcc tcc tca tcc aca gct gtc 1167

Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val

350

355

360

ata gtc tca gcc cgc atg gcc ccc gag gag atc atc atg gac aga ccc 1215

Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro

365

370

375

380

ttc ctc ttt gtg gtc cgg cac aac ccc aca gga aca gtc ctt ttc atg 1263

Phe Leu Phe Val Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met

385

390

395

ggc caa gtg atg gaa ccc tgaccctggg gaaagacgcc ttcattctggg 1311

Gly Gln Val Met Glu Pro

400

acaaaactgg agatgcatcg ggaaagaaga aactccgaag aaaagaattt tagtgtaaat 1371

gactctttct gaaggaagag aagacatttg ccttttgta aaagatggta aaccagatct 1431

gtctccaaga ccttggcctc tccctggagg acccttaggt caaactccct agtctccacc 1491

tgagaccctg ggagagaagt ttgaagcaca actcccttaa ggctccaaa ccagacggtg 1551

acgcctgcgg gaccatctgg ggcacctgct tccaccgctc tccttgccca ctcggtctg 1611

cagacctggt tcccactgag gcccttgca ggaatggaact acggggctta caggagcttt 1671

tgtgtgacct giagaaacta ttctgttcc agtcacatg ccatcactct tgtactgcct 1731

gccaccgcgg aggaggctgg tgacaggcca aaggccagtg gaagaaacac ccttcatct 1791

cagagtccac tgtggcactg gccacccctc cccagtacag gggctgca ggtggcagag 1851

tgaatgtccc ccatcatgtg gccaactct cctggcctgg ccatctccct cccagaaac 1911

agtgatcatg ggtaattttg gagtgiaggt gacttgitta ccatatgaag cagattctg 1971

cttcccttta ttttatagg aatagaggaa gaaatgtcag atgcgtgccc agctcttcac 2031



cccccaatct ctiggigggg aggggtgtac ctaaataatt atcatacct tgcccttgag 2091  
tgcttgtag agagaaagag aactactaag gaaaataata ttatttaaac tcgctcctag 2151  
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gaagc 2876

<210> 88

<211> 402

<212> PRT

<213> Homo sapiens

<400> 88

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Val	Phe	Gly	Glu	Gly	Ser	Ala	Val	His	His	Pro	Pro	Ser	Tyr	Val	Ala
1															
His	Leu	Ala	Ser	Asp	Phe	Gly	Val	Arg	Val	Phe	Gln	Gln	Val	Ala	Gln
Ala	Ser	Lys	Asp	Arg	Asn	Val	Val	Phe	Ser	Pro	Tyr	Gly	Val	Ala	Ser

35	40	45
Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln		
50	55	60
Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro		
65	70	75
Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp		
85	90	95
Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu		
100	105	110
Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val		
115	120	125
Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn		
130	135	140
Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly		
145	150	155
Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu		
165	170	175
Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His		
180	185	190
Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met		
195	200	205
Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp		
210	215	220
Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu		
225	230	235
Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala		

245	250	255
Leu Thr Asn Ile Leu Ser Ala Gln	Leu Ile Ser His Trp Lys Gly Asn	
260	265	270
Met Thr Arg Leu Pro Arg Leu Leu Val	Leu Pro Lys Phe Ser Leu Glu	
275	280	285
Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn	Leu Gly Met Thr Asp	
290	295	300
Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu		
305	310	315
Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn		
325	330	335
Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala		
340	345	350
Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val		
355	360	365
Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met		
370	375	380
Glu Pro		
385		

<210> 89

<211> 1412

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (52).. (1341)

<400> 89

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Met Ser

1

ttc acc act cgc tcc acc ttc tcc acc aac tac cgg tcc ctg ggc tct 105

Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu Gly Ser

5

10

15

gtc cag gcg ccc agc tac ggc gcc cgg ccg gtc agc agc gcg gcc agc 153

Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala Ala Ser

20

25

30

gtc tat gca ggc gct ggg ggc tct ggt tcc cgg atc tcc gtg tcc cgc 201

Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val Ser Arg

35

40

45

50

tcc acc agc ttc agg ggc ggc atg ggg tcc ggg ggc ctg gcc acc ggg 249

Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr Gly

55

60

65

ata gcc ggg ggt ctg gca gga atg gga ggc atc cag aac gag aag gag 297

Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys Glu

70

75

80

acc atg caa agc ctg aac gac cgc ctg gcc tct tac ctg gac aga gtg 345

Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg Val

85

90

95

agg agc ctg gag acc gag aac cgg agg ctg gag agc aaa atc cgg gag 393

Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg Glu

100

105

110

cac ttg gag aag aag gga ccc cag gtc aga gac tgg agc cat tac ttc 441

His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr Phe

115	120	125	130	
aag atc atc gag gac ctg agg gct cag atc ttc gca aat act gtg gac	489			
Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val Asp				
135	140	145		
aat gcc cgc atc gtt ctg cag att gac aat gcc cgt ctt gct gct gat	537			
Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala Asp				
150	155	160		
gac ttt aga gtc aag tat gag aca gag ctg gcc atg cgc cag tct gtg	585			
Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser Val				
165	170	175		
gag aac gac atc cat ggg ctc cgc aag gtc att gat gac acc aat atc	633			
Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn Ile				
180	185	190		
aca cga ctg cag ctg gag aca gag atc gag gct ctc aag gag gag ctg	681			
Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu Leu				
195	200	205	210	
ctc ttc atg aag aag aac cac gaa gag gaa gta aaa ggc cta caa gcc	729			
Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln Ala				
215	220	225		
cag att gcc agc tct ggg ttg acc gtg gag gta gat gcc ccc aaa tct	777			
Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys Ser				
230	235	240		
cag gac ctc gcc aag atc atg gca gac atc cgg gcc caa tat gac gag	825			
Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp Glu				
245	250	255		
ctg gct cgg aag aac cga gag gag cta gac aag tac tgg tct cag cag	873			

Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln Gln	
260	265
270	
att gag gag agc acc aca gig gtc acc aca cag tct gct gag gtt gga	921
Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val Gly	
275	280
285	290
gct gct gag acg acg ctc aca gag ctg aga cgt aca gtc cag tcc ttg	969
Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser Leu	
295	300
305	
gag atc gac ctg gac tcc atg aga aat ctg aag gcc agc ttg gag aac	1017
Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu Asn	
310	315
320	
agc ctg agg gag gtg gag gcc cgc tac gcc cta cag atg gag cag ctc	1065
Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln Leu	
325	330
335	
aac ggg atc ctg ctg cac ctt gag tca gag ctg gca cag acc cgg gca	1113
Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg Ala	
340	345
350	
gag gga cag cgc cag gcc cag gag tat gag gcc ctg ctg aac atc aag	1161
Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile Lys	
355	360
365	370
gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa gat	1209
Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Asp	
375	380
385	
ggc gag gac ttt aat ctt ggt gat gcc ttg gac agc agc aac tcc atg	1257
Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser Met	
390	395
400	
caa acc atc caa aag acc acc acc cgc cgg ata gtg gat ggc aaa gtg	1305

Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys Val  
405 410 415  
gtg tct gag acc aat gac acc aaa gtt ctg agg cat taagccagca 1351  
Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His  
420 425 430  
gaagcagggt accctttggg gagcaggagg ccaataaaaa gttcagagtt cattggatgt 1411  
c 1412

<210> 90  
<211> 430  
<212> PRT  
<213> Homo sapiens  
<400> 90

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20 25 30  
Ala Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val  
35 40 45  
Ser Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala  
50 55 60  
Thr Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu  
65 70 75 80  
Lys Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp  
85 90 95  
Arg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile  
100 105 110

Arg Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His  
 115 120 125  
 Tyr Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr  
 130 135 140  
 Val Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala  
 145 150 155 160  
 Ala Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln  
 165 170 175  
 Ser Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr  
 180 185 190  
 Asn Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu  
 195 200 205  
 Glu Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu  
 210 215 220  
 Gln Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro  
 225 230 235 240  
 Lys Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr  
 245 250 255  
 Asp Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser  
 260 265 270  
 Gln Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu  
 275 280 285  
 Val Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln  
 290 295 300  
 Ser Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu  
 305 310 315 320



Glu Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu

325

330

335

Gln Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr

340

345

350

Arg Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn

355

360

365

Ile Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu

370

375

380

Glu Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn

385

390

395

400

Ser Met Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly

405

410

415

Lys Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His

420

425

430

<210> 91

<211> 1040

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (171).. (968)

<400> 91

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tictttgaag gagatgctaa gtttggggaa agaaacgaag ggagcggaca aggaggagaa 120

ggtgcctgaa tgggaacccc ccgaagcgcc tgaaaaggag agacaggagg atg atg 176

Met Met

tcc cag ctg gag ctg ctg agt ggg gga gag atg ctg tgc ggt ggc ttc 224  
 Ser Gln Leu Glu Leu Leu Ser Gly Gly Glu Met Leu Cys Gly Gly Phe  
           5                    10                    15  
 tac cct cgg ctg tcc tgc tgc ctg cgg agt gac agc ccg ggg cta ggg 272  
 Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly Leu Gly  
           20                    25                    30  
 cgc ctg gag aat aag ata ttt tct gtt acc aac aac aca gaa tgt ggg 320  
 Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu Cys Gly  
           35                    40                    45                    50  
 aag tta ctg gag gaa atc aaa tgt gca ctt tgc tct cca cat tct caa 368  
 Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His Ser Gln  
                     55                    60                    65  
 agc ctg ttc cac tca cct gag aga gaa gtc ttg gaa aga gac cta gta 416  
 Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp Leu Val  
           70                    75                    80  
 ctt cct ctg ctg tgc aaa gac tat tgc aaa gaa ttc ttt tac act tgc 464  
 Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr Thr Cys  
           85                    90                    95  
 cga ggc cat att cca ggt ttc ctt caa aca act gcg gat gag ttt tgc 512  
 Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu Phe Cys  
           100                    105                    110  
 ttt tac tat gca aga aaa gat ggt ggg ttg tgc ttt cca gat ttt cca 560  
 Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp Phe Pro  
           115                    120                    125                    130  
 aga aaa caa gtc aga gga cca gca tct aac tac ttg gac cag atg gaa 608  
 Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln Met Glu

135	140	145	
gaa tat gac aaa gtg gaa gag atc agc aga aag cac aaa cac aac tgc			656
Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His Asn Cys			
150	155	160	
ttc tgt att cag gag gtt gtg agt ggg ctg cgg cag ccc gtt ggt gcc			704
Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val Gly Ala			
165	170	175	
ctg cat agt ggg gat ggc tcg caa cgt ctc ttc att ctg gaa aaa gaa			752
Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu Lys Glu			
180	185	190	
ggc tat gtg aag ata ctt acc cct gaa gga gaa att ttc aag gag cct			800
Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro			
195	200	205	210
tat ttg gac att cac aaa ctt gtt caa agt gga ata aag gtt ggc ttt			848
Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val Gly Phe			
215	220	225	
tta aat ttt att tat ttt tgt gct ggc tac gtt aat ttt att tta gtg			896
Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile Leu Val			
230	235	240	
tta cct tcc tca ctg aag gta ttt ctt tgt aat aaa aga aag aat ctt			944
Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys Asn Leu			
245	250	255	
gca gga gaa aat aag ggg gca aca taagaaacaa taattatggc accigaatt			998
Ala Gly Glu Asn Lys Gly Ala Thr			
260	265		
ggacagtgc attaaakgtt ggctktttaw attttaaaaa aa			1040

<210> 92

<211> 266

<212> PRT

<213> Homo sapiens

<400> 92

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Gly Phe Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly  
20 25 30  
Leu Gly Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu  
35 40 45  
Cys Gly Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His  
50 55 60  
Ser Gln Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp  
65 70 75 80  
Leu Val Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr  
85 90 95  
Thr Cys Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu  
100 105 110  
Phe Cys Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp  
115 120 125  
Phe Pro Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln  
130 135 140  
Met Glu Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His  
145 150 155 160  
Asn Cys Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val

165	170	175
Gly Ala Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu		
180	185	190
Lys Glu Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys		
195	200	205
Glu Pro Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val		
210	215	220
Gly Phe Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile		
225	230	235
Leu Val Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys		
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Asn Leu Ala Gly Glu Asn Lys Gly Ala Thr		
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<210> 93

<211> 1639

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75).. (371)

<400> 93

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      Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala
          1           5           10
ttc ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt 158

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Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser  
15 20 25  
gct aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc 206  
Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe  
30 35 40  
cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac 254  
His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His  
45 50 55 60  
tgc gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc 302  
Cys Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu  
65 70 75  
tgt ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt 350  
Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe  
80 85 90  
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Leu Lys Arg Ala Glu Asn Ser  
95  
aatcagtgaa gatgccagt aaacttcaag caaatctact tcaacacttc atgtattgtg 461  
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tgccttgggt tctcctttat ttctaagtgg aaaaagtatt agccaccatc ttacctcaca 941  
gtgatgttgt gaggacatgt ggaagcactt taagtitttt catcataaca taaattattt 1001

tcaagtgtaa cttattaacc tatttattat ttatgtatit atttaagcat caaatatttg 1061  
tgcaagaatt tggaaaaata gaagatgaat cattgattga atagttataa agatgttata 1121  
gtaaaattat tttattttag atattaaaig atgttttatt agataaattt caatcagggt 1181  
ttttagatta aacaaagaaa caattgggia cccagttaaa ttttcatttc agataaacia 1241  
caaataattt tttagtataa gtacattatt gtttatctga aagttttaat tgaactaaca 1301  
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<210> 94

<211> 99

<212> PRT

<213> Homo sapiens

<400> 94

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Ala	Ala	Leu	Cys	Glu	Gly	Ala	Val	Leu	Pro	Arg	Ser	Ala	Lys	Glu	Leu
1				5						10					15
Arg	Cys	Gln	Cys	Ile	Lys	Thr	Tyr	Ser	Lys	Pro	Phe	His	Pro	Lys	Phe
				20						25					30
Ile	Lys	Glu	Leu	Arg	Val	Ile	Glu	Ser	Gly	Pro	His	Cys	Ala	Asn	Thr
				35						40					45
Glu	Ile	Ile	Val	Lys	Leu	Ser	Asp	Gly	Arg	Glu	Leu	Cys	Leu	Asp	Pro
				50						55					60
Lys	Glu	Asn	Trp	Val	Gln	Arg	Val	Val	Glu	Lys	Phe	Leu	Lys	Arg	Ala

65	70	75	80
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Glu Asn Ser

<210> 95

<211> 3293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (8).. (1945)

<400> 95

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Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala	
1 5 10	
tgc tgc tgc tgt cct cgc gtc gcg ggt gtg ccc gga gag gct gag cag	97
Cys Cys Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln	
15 20 25 30	
cct gcg cct gag ctg gtg gag gtg gaa gtg ggc agc aca gcc ctt ctg	145
Pro Ala Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu	
35 40 45	
aag tgc ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg	193
Lys Cys Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp	
50 55 60	
ttt tct gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag	241
Phe Ser Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln	
65 70 75	
ggc cag ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc	289



Gly Gln Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu	
80	85
cag gac aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac	337
Gln Asp Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp	
95	100
gag cgc atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac	385
Glu Arg Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr	
115	120
cgc atc cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag	433
Arg Ile Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln	
130	135
gtc aac ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc	481
Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val	
145	150
gct acc tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg	529
Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp	
160	165
tac aag aat ggc cgg cct ctg aag gag gag aag aac cgg gtc cac att	577
Tyr Lys Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile	
175	180
cag tcg tcc cag act gtg gag tcg agt ggt ttg tac acc ttg cag agt	625
Gln Ser Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser	
195	200
att ctg aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac	673
Ile Leu Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr	
210	215
	220

tgt gag ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc	721
Cys Glu Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser	
225 230 235	
agg gaa gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtg tgg ctg	769
Arg Glu Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu	
240 245 250	
gaa gtg gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc	817
Glu Val Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile	
255 260 265 270	
agg tgt ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag	865
Arg Cys Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys	
275 280 285	
cag aac ccc agc acc agg gag gca gag gaa gag aca acc aac gac aac	913
Gln Asn Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn	
290 295 300	
ggg gtc ctg gtg ctg gag cct gcc cgg aag gaa cac agt ggg cgc tat	961
Gly Val Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr	
305 310 315	
gaa tgt cag gcc tgg aac ttg gac acc atg ata tcg ctg ctg agt gaa	1009
Glu Cys Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu	
320 325 330	
cca cag gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc	1057
Pro Gln Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro	
335 340 345 350	
gca gcc cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag	1105
Ala Ala Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu	
355 360 365	

gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca	1153
Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr	
370 375 380	
gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa	1201
Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys	
385 390 395	
cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata	1249
Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile	
400 405 410	
ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc	1297
Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro	
415 420 425 430	
cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg	1345
Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met	
435 440 445	
gtg ttg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc	1393
Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile	
450 455 460	
tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag	1441
Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln	
465 470 475	
cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag	1489
Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu	
480 485 490	
aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc	1537
Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser	

495	500	505	510	
atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc				1585
Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser				
	515	520	525	
aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga				1633
Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg				
	530	535	540	
gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg				1681
Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg				
	545	550	555	
ggc gtg gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg				1729
Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val				
	560	565	570	
ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc				1777
Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys				
575	580	585	590	
agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc				1825
Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr				
	595	600	605	
gaa ctt gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc				1873
Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly				
	610	615	620	
ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga				1921
Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly				
	625	630	635	
gag aaa tac atc gat ctg agg cat tagccccgaa tcacttcagc tcccttcct				1975
Glu Lys Tyr Ile Asp Leu Arg His				

640

645

gccitggacca ttcccagctc ccigctcact ctctctcag ccaaagctca aagggactag 2035  
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 ccigaggacc tcacttggcc ctgcaaggcc cgcctttcag ggaccagtc accaccatct 2155  
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&lt;210&gt; 96

&lt;211&gt; 646

&lt;212&gt; PRT

<213> Homo sapiens

<400> 96

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				20					25					30	
Pro	Glu	Leu	Val	Glu	Val	Glu	Val	Gly	Ser	Thr	Ala	Leu	Leu	Lys	Cys
				35				40						45	
Gly	Leu	Ser	Gln	Ser	Gln	Gly	Asn	Leu	Ser	His	Val	Asp	Trp	Phe	Ser
				50				55						60	
Val	His	Lys	Glu	Lys	Arg	Thr	Leu	Ile	Phe	Arg	Val	Arg	Gln	Gly	Gln
				65				70						75	
Gly	Gln	Ser	Glu	Pro	Gly	Glu	Tyr	Glu	Gln	Arg	Leu	Ser	Leu	Gln	Asp
				85				90						95	
Arg	Gly	Ala	Thr	Leu	Ala	Leu	Thr	Gln	Val	Thr	Pro	Gln	Asp	Glu	Arg
				100				105						110	
Ile	Phe	Leu	Cys	Gln	Gly	Lys	Arg	Pro	Arg	Ser	Gln	Glu	Tyr	Arg	Ile
				115				120						125	
Gln	Leu	Arg	Val	Tyr	Lys	Ala	Pro	Glu	Glu	Pro	Asn	Ile	Gln	Val	Asn
				130				135						140	
Pro	Leu	Gly	Ile	Pro	Val	Asn	Ser	Lys	Glu	Pro	Glu	Glu	Val	Ala	Thr
				145				150						155	
Cys	Val	Gly	Arg	Asn	Gly	Tyr	Pro	Ile	Pro	Gln	Val	Ile	Trp	Tyr	Lys
				165				170						175	
Asn	Gly	Arg	Pro	Leu	Lys	Glu	Glu	Lys	Asn	Arg	Val	His	Ile	Gln	Ser
				180				185						190	

Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu  
 195 200 205  
 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu  
 210 215 220  
 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu  
 225 230 235 240  
 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val  
 245 250 255  
 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys  
 260 265 270  
 Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn  
 275 280 285  
 Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val  
 290 295 300  
 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys  
 305 310 315 320  
 Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln  
 325 330 335  
 Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala  
 340 345 350  
 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu  
 355 360 365  
 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln  
 370 375 380  
 Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu  
 385 390 395 400  
 Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly

405	410	415	
Leu Asn Arg Thr Gln Leu Val Lys	Leu Ala Ile Phe Gly Pro Pro Trp		
420	425	430	
Met Ala Phe Lys Glu Arg Lys Val Trp	Val Lys Glu Asn Met Val Leu		
435	440	445	
Asn Leu Ser Cys Glu Ala Ser Gly His Pro	Arg Pro Thr Ile Ser Trp		
450	455	460	
Asn Val Asn Gly Thr Ala Ser Glu Gln Asp	Gln Asp Pro Gln Arg Val		
465	470	475	480
Leu Ser Thr Leu Asn Val Leu Val Thr Pro	Glu Leu Leu Glu Thr Gly		
485	490	495	
Val Glu Cys Thr Ala Ser Asn Asp Leu Gly	Lys Asn Thr Ser Ile Leu		
500	505	510	
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu	Thr Pro Asp Ser Asn Thr		
515	520	525	
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser	Pro His Thr Arg Ala Asn		
530	535	540	
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu	Pro Glu Ser Arg Gly Val		
545	550	555	560
Val Ile Val Ala Val Ile Val Cys Ile Leu	Val Leu Ala Val Leu Gly		
565	570	575	
Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly	Lys Leu Pro Cys Arg Arg		
580	585	590	
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro	Ser Arg Lys Thr Glu Leu		
595	600	605	
Val Val Glu Val Lys Ser Asp Lys Leu Pro	Glu Glu Met Gly Leu Leu		



610	615	620	
Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys			
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Tyr Ile Asp Leu Arg His			

645

<210> 97  
 <211> 1642  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
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 <222> (158).. (1279)  
 <400> 97

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 ggggaccagc agctgtcgcc gccgcctca gggatgaagag ggaacagaaa tctttgcccc 120  
 ctgacitttg aaatctcgtt taaccttcaa actggcg atg tca agg gtt cca agt 175

Met Ser Arg Val Pro Ser

1 5

cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223

Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp

10 15 20

tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271

Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile

25 30 35

aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319

Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser

40	45	50	
tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga	367		
Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg			
55	60	65	70
gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt	415		
Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu			
75	80	85	
tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cgg gca aaa ttc	463		
Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe			
90	95	100	
aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag	511		
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu			
105	110	115	
agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag	559		
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys			
120	125	130	
aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc	607		
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu			
135	140	145	150
cct gat gac aag ctt acc ctc ttc tgc gag gtg agt gtt gtg caa gat	655		
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp			
155	160	165	
tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct	703		
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro			
170	175	180	
gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg	751		
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg			

185	190	195	
ttc aca gac tgc tgc ttg tgt gtt gcc ggc cag gaa ttc cag gct cac	799		
Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His			
200	205	210	
aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa	847		
Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu			
215	220	225	230
cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg	895		
His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val			
235	240	245	
gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag	943		
Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys			
250	255	260	
gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac	991		
Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp			
265	270	275	
aag tat gcc ctg gag cgc tta aag gtc atg tgt gag gat gcc ctc tgc	1039		
Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys			
280	285	290	
agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac	1087		
Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp			
295	300	305	310
ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac	1135		
Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn			
315	320	325	
tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg	1183		

Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val

330

335

340

gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca 1231

Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser

345

350

355

gca cag tgc cct ttt ctg gga ccc cca cgc aaa cgc ctg aag caa tcc 1279

Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser

360

365

370

taagatcctg ctgtttgtaa gactccgttt aatttccaga agcagcagcc actgttgctg 1339

ccactgacca ccaggtagac agcgcaatct gaggagcttt tactctgttg tgaggggaag 1399

agactgcatt ggggccccag acttttaaaa cagcactaaa taacttgggg gaaacggggg 1459

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agg 1642

<210> 98

<211> 374

<212> PRT

<213> Homo sapiens

<400> 98

Met Ser Arg Val Pro Ser Pro Pro Pro Ala Glu Met Ser Ser Gly

1

5

10

15

Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe

20

25

30

Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met

35

40

45

Gly	Glu	Val	Ile	Lys	Ser	Ser	Thr	Phe	Ser	Ser	Gly	Ala	Asn	Asp	Lys
50				55				60							
Leu	Lys	Trp	Cys	Leu	Arg	Val	Asn	Pro	Lys	Gly	Leu	Asp	Glu	Glu	Ser
65				70				75				80			
Lys	Asp	Tyr	Leu	Ser	Leu	Tyr	Leu	Leu	Leu	Val	Ser	Cys	Pro	Lys	Ser
85				90				95							
Glu	Val	Arg	Ala	Lys	Phe	Lys	Phe	Ser	Ile	Leu	Asn	Ala	Lys	Gly	Glu
100				105				110							
Glu	Thr	Lys	Ala	Met	Glu	Ser	Gln	Arg	Ala	Tyr	Arg	Phe	Val	Gln	Gly
115				120				125							
Lys	Asp	Trp	Gly	Phe	Lys	Lys	Phe	Ile	Arg	Arg	Asp	Phe	Leu	Leu	Asp
130				135				140							
Glu	Ala	Asn	Gly	Leu	Leu	Pro	Asp	Asp	Lys	Leu	Thr	Leu	Phe	Cys	Glu
145				150				155				160			
Val	Ser	Val	Val	Gln	Asp	Ser	Val	Asn	Ile	Ser	Gly	Gln	Asn	Thr	Met
165				170				175							
Asn	Met	Val	Lys	Val	Pro	Glu	Cys	Arg	Leu	Ala	Asp	Glu	Leu	Gly	Gly
180				185				190							
Leu	Trp	Glu	Asn	Ser	Arg	Phe	Thr	Asp	Cys	Cys	Leu	Cys	Val	Ala	Gly
195				200				205							
Gln	Glu	Phe	Gln	Ala	His	Lys	Ala	Ile	Leu	Ala	Ala	Arg	Ser	Pro	Val
210				215				220							
Phe	Ser	Ala	Met	Phe	Glu	His	Glu	Met	Glu	Glu	Ser	Lys	Lys	Asn	Arg
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Val	Glu	Ile	Asn	Asp	Val	Glu	Pro	Glu	Val	Phe	Lys	Glu	Met	Met	Cys
245				250				255							
Phe	Ile	Tyr	Thr	Gly	Lys	Ala	Pro	Asn	Leu	Asp	Lys	Met	Ala	Asp	Asp

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 Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met  
 275                      280                      285  
 Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu  
 290                      295                      300  
 Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln  
 305                      310                      315                      320  
 Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser  
 325                      330                      335  
 Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala  
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Met Gly

ctg gcc tgg gga cta ggc gtc ctg ttc ctg atg cat gig tgt ggc acc	165
Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr	
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aac cgc att cca gag tct ggc gga gac aac agc gtg ttt gac atc ttt	213
Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp Ile Phe	
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gaa ctc acc ggg gcc gcc cgc aag ggg tct ggg cgc cga ctg gtg aag	261
Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu Val Lys	
35 40 45 50	
ggc ccc gac cct tcc agc cca gct ttc cgc atc gag gat gcc aac ctg	309
Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala Asn Leu	
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atc ccc cct gtg cct gat gac aag ttc caa gac ctg gtg gat gct gtg	357
Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp Ala Val	
70 75 80	
cgg gca gaa aag ggt ttc ctc ctt ctg gca tcc ctg agg cag atg aag	405
Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln Met Lys	
85 90 95	
aag acc cgg ggc acg ctg ctg gcc ctg gag cgg aaa gac cac tct ggc	453
Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His Ser Gly	
100 105 110	
cag gtc ttc agc gtg gtg tcc aat ggc aag gcg ggc acc ctg gac ctc	501
Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu Asp Leu	
115 120 125 130	
agc ctg acc gtc caa gga aag cag cac gtg gtg tct gtg gaa gaa gct	549





Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg Thr Ile	
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285	290
gtg acc acg ctg cag gac agc atc cgc aaa gtg act gaa gag aac aaa	1029
Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu Asn Lys	
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gag ttg gcc aat gag ctg agg cgg cct ccc cta tgc tat cac aac gga	1077
Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly	
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gtt cag tac aga aat aac gag gaa tgg act gtt gat agc tgc act gag	1125
Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys Thr Glu	
325	330
335	
tgt cac tgt cag aac tca gtt acc atc tgc aaa aag gtg tcc tgc ccc	1173
Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser Cys Pro	
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atc atg ccc tgc tcc aat gcc aca gtt cct gat gga gaa tgc tgt cct	1221
Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys Cys Pro	
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365	370
cgc tgt tgg ccc agc gac tct gcg gac gat ggc tgg tct cca tgg tcc	1269
Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro Trp Ser	
375	380
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gag tgg acc tcc tgt tct acg agc tgt ggc aat gga att cag cag cgc	1317
Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln Gln Arg	
390	395
400	
ggc cgc tcc tgc gat agc ctc aac aac cga tgt gag ggc tcc tcg gtc	1365
Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser Ser Val	
405	410
415	

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Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe Lys Gln	
420 425 430	
gat ggt ggc tgg agc cac tgg tcc ccg tgg tca tct tgt tct gtg aca	1461
Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr	
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Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser	
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ccc cag atg aat ggg aaa ccc tgt gaa ggc gaa gcg cgg gag acc aaa	1557
Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys	
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Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly Pro Trp	
485 490 495	
tca cca tgg gac atc tgt tct gtc acc tgt gga gga ggg gta cag aaa	1653
Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val Gln Lys	
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cgt agt cgt ctc tgc aac aac ccc gca ccc cag ttt gga ggc aag gac	1701
Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly Lys Asp	
515 520 525 530	
tgc gtt ggt gat gta aca gaa aac cag atc tgc aac aag cag gac tgt	1749
Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys	
535 540 545	
cca att gat gga tgc ctg tcc aat ccc tgc ttt gcc ggc gtg aag tgt	1797
Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys	
550 555 560	

act agc tac cct gat ggc agc tgg aaa tgt ggt gct tgt ccc cct ggt	1845
Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro Pro Gly	
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Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys Lys Glu	
580 585 590	
gtg cct gat gcc tgc ttc aac cac aat gga gag cac cgg tgt gag aac	1941
Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys Glu Asn	
595 600 605 610	
acg gac ccc ggc tac aac tgc ctg ccc tgc ccc cca cgc ttc acc ggc	1989
Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe Thr Gly	
615 620 625	
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Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn Lys Gln	
630 635 640	
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Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn	
645 650 655	
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Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr	
660 665 670	
cgc tgc gag tgc aag cct ggc tac gct ggc aat ggc atc atc tgc ggg	2181
Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly	
675 680 685 690	
gag gac aca gac ctg gat ggc tgg ccc aat gag aac ctg gtg tgc gtg	2229
Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val	

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Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro			
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aac tca ggg cag gaa gac tat gac aag gat gga att ggt gat gcc tgt			2325
Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys			
725	730	735	
gat gat gac gat gac aat gat aaa att cca gat gac agg gac aac tgt			2373
Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys			
740	745	750	
cca ttc cat tac aac cca gct cag tat gac tat gac aga gat gat gtg			2421
Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val			
755	760	765	770
gga gac cgc tgt gac aac tgt ccc tac aac cac aac cca gat cag gca			2469
Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala			
775	780	785	
gac aca gac aac aat ggg gaa gga gac gcc tgt gct gca gac att gat			2517
Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp			
790	795	800	
gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat			2565
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn			
805	810	815	
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Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp			
820	825	830	
aat tgc ccc ttg gaa cac aat ccg gat cag ctg gac tct gac tca gac			2661
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp			

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cgc att gga gat acc tgt gac aac aat cag gat att gat gaa gat ggc	2709			
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly				
855	860	865		
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag	2757			
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln				
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gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat	2805			
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp				
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900	905	910		
aat ccc gac cag aag gac tct gac ggc gat ggt cga ggt gat gcc tgc	2901			
Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys				
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aaa gat gat ttt gac cat gac agt gtg cca gac atc gat gac atc tgt	2949			
Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys				
935	940	945		
cct gag aat gtt gac atc agt gag acc gat ttc cgc cga ttc cag atg	2997			
Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met				
950	955	960		
att cct ctg gac ccc aaa ggg aca tcc caa aat gac cct aac tgg gtt	3045			
Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val				
965	970	975		
gta cgc cat cag ggt aaa gaa ctc gtc cag act gtc aac tgt gat cct	3093			

Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro	
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Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe Ser Gly	
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acc ttc ttc atc aac acc gaa agg gac gat gac tat gct gga ttt gtc	3189
Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly Phe Val	
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ttt ggc tac cag tcc agc agc cgc ttt tat gtt gtg atg tgg aag caa	3237
Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln	
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gtc acc cag tcc tac tgg gac acc aac ccc acg agg gct cag gga tac	3285
Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln Gly Tyr	
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Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro Gly Glu	
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cac ctg cgg aac gcc ctg tgg cac aca gga aac acc cct ggc cag gtg	3381
His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val	
1075	1080
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cgc acc ctg tgg cat gac cct cgt cac ata ggc tgg aaa gat ttc acc	3429
Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp Phe Thr	
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Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg	
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Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile

1125

1130

1135

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Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser

1140

1145

1150

caa gaa atg gtg ttc ttc tct gac ctg aaa tac gaa tgt aga gat ccc 3621

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1155

1160

1165

1170

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Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp			
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Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln			
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Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His			
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Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu			
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Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu			
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Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val			
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Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn			
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Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala			
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Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe			
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Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu			
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Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu			
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Asn	Tyr	Ile	Gly	His	Lys	Thr	Lys	Asp	Leu	Gln	Ala	Ile	Cys	Gly	Ile
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Ser	Cys	Asp	Glu	Leu	Ser	Ser	Met	Val	Leu	Glu	Leu	Arg	Gly	Leu	Arg
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Thr	Ile	Val	Thr	Thr	Leu	Gln	Asp	Ser	Ile	Arg	Lys	Val	Thr	Glu	Glu
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Trp	Ser	Glu	Trp	Thr	Ser	Cys	Ser	Thr	Ser	Cys	Gly	Asn	Gly	Ile	Gln
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Gln	Arg	Gly	Arg	Ser	Cys	Asp	Ser	Leu	Asn	Asn	Arg	Cys	Glu	Gly	Ser
									405						415
Ser	Val	Gln	Thr	Arg	Thr	Cys	His	Ile	Gln	Glu	Cys	Asp	Lys	Arg	Phe
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Lys	Gln	Asp	Gly	Gly	Trp	Ser	His	Trp	Ser	Pro	Trp	Ser	Ser	Cys	Ser
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Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly			
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Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly			
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Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln			
530	535	540	
Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val			
545	550	555	560
Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro			
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Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys			
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Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys			
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Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe			
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Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn			
625	630	635	640
Lys Gln Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp			
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Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro			

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Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile			
675	680	685	
Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val			
690	695	700	
Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn			
705	710	715	720
Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp			
725	730	735	
Ala Cys Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp			
740	745	750	
Asn Cys Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp			
755	760	765	
Asp Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp			
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Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp			
785	790	795	800
Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val			
805	810	815	
Tyr Asn Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln			
820	825	830	
Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp			
835	840	845	
Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu			
850	855	860	
Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala			

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Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His			
	885	890	895
Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu			
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Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp			
	915	920	925
Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp			
	930	935	940
Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe			
945	950	955	960
Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn			
	965	970	975
Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys			
	980	985	990
Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe			
	995	1000	1005
Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly			
	1010	1015	1020
Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp			
1025	1030	1035	1040
Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln			
	1045	1050	1055
Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro			
	1060	1065	1070
Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly			
	1075	1080	1085

Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp

1090

1095

1100

Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe

1105

1110

1115

1120

Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly

1125

1130

1135

Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val

1140

1145

1150

Phe Ser Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg

1155

1160

1165

Asp Pro

1170

<210> 101

<211> 838

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35).. (568)

<400> 101

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Met Ser Gly Gly Lys Tyr Val

1

5

gac tcg gag gga cat ctc tac acc gtt ccc atc cgg gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

10

15

20

atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag	151
Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys	
25 30 35	
caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac	199
Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp	
40 45 50 55	
cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg	247
Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val	
60 65 70	
att gca gaa cca gaa ggg aca cac agt ttt cac ggc att tgg aag gcc	295
Ile Ala Glu Pro Glu Gly Thr His Ser Phe His Gly Ile Trp Lys Ala	
75 80 85	
agc ttc acc acc ttc act gtg acg aaa tac tgg ttt tac cgc ttg ctg	343
Ser Phe Thr Thr Phe Thr Val Thr Lys Tyr Trp Phe Tyr Arg Leu Leu	
90 95 100	
tct gcc ctc ttt ggc atc ccg atg gca ctc atc tgg ggc att tac ttc	391
Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe	
105 110 115	
gcc att ctc tct ttc ctg cac atc tgg gca gtt gta cca tgc att aag	439
Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys	
120 125 130 135	
agc ttc ctg att gag att cag tgc acc agc cgt gtc tat tcc atc tac	487
Ser Phe Leu Ile Glu Ile Gln Cys Thr Ser Arg Val Tyr Ser Ile Tyr	
140 145 150	
gtc cac acc gtc tgt gac cca ctc ttt gaa gct gtt ggg aaa ata ttc	535
Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe	

155 160 165  
 agc aat gtc cgc atc aac ttg cag aaa gaa ata taaatgacat ttcaaggata 588  
 Ser Asn Val Arg Ile Asn Leu Gln Lys Glu Ile

170 175  
 gaagtatacc tgatTTTTTT tccTTTTaat tttcctgggtg ccaatttcaa gtccaagtt 648  
 gctaatacag caacgaattt atgaattgaa ttatcttgggt tgaataataa aagatcactt 708  
 tctcagtttt cataagtatt atgtctcttc tgagctatTTT catctatTTT tggcagtcgt 768  
 aatTTTTTaaa acccatttat atttctttcc ttacctTTTT atttgcattgt ggatcaacca 828  
 tcgctttatt 838

<210> 102

<211> 178

<212> PRT

<213> Homo sapiens

<400> 102

Met Ser Gly Gly Lys Tyr Val Asp Ser Glu Gly His Leu Tyr Thr Val  
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 Pro Ile Arg Glu Gln Gly Asn Ile Tyr Lys Pro Asn Asn Lys Ala Met  
 20 25 30  
 Ala Asp Glu Leu Ser Glu Lys Gln Val Tyr Asp Ala His Thr Lys Glu  
 35 40 45  
 Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp Asp Val Val  
 50 55 60  
 Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser  
 65 70 75 80  
 Phe His Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys  
 85 90 95



Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala  
                   100                  105                  110  
 Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp  
                   115                  120                  125  
 Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Thr  
                   130                  135                  140  
 Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe  
 145                  150                  155                  160  
 Glu Ala Val Gly Lys Ile Phe Ser Asn Val Arg Ile Asn Leu Gln Lys  
                   165                  170                  175

Glu Ile

<210> 103

<211> 2269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (444)

<400> 103

ccg ccc gcc acc agc tac gcc ccg tcc gac glg ccc tcg ggg gtc gcg 48

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1                  5                  10                  15

ctg ttc ctc acc atc cct ttc gcc ttc ttc ctg ccc gag ctg ata ttt 96

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20                  25                  30

ggg ttc ttg gtc tgg acc atg gta gcc gcc acc cac ata gta tac ccc 144

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro  
 35 40 45  
 ttg ctg caa gga tgg gtg atg tat gtc tgc ctc acc tgc ttt ctc atc 192  
 Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile  
 50 55 60  
 tcc ttg atg ttc ctg ttg tct tac ttg ttt gga ttt tac aaa aga ttt 240  
 Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe  
 65 70 75 80  
 gaa tcc tgg aga gtt ctg gac agc ctg tac cac ggg acc act ggc atc 288  
 Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile  
 85 90 95  
 ctg tac atg agc gct gcc gtc cta caa gta cat gcc acg att gtt tct 336  
 Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser  
 100 105 110  
 gag aaa ctg ctg gac cca aga att tac tac att aat tgc gca gcc tgc 384  
 Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser  
 115 120 125  
 ttc ttc gcc ttc atc gcc acg ctg ctc tac att ctc cat gcc ttc agc 432  
 Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser  
 130 135 140  
 atc tat tac cac tgatgcacag gcgccaggcc aagggggaaa tgctctttga 484  
 Ile Tyr Tyr His  
 145  
 aagctccaat tatiggtccc caaaagcagc ttccaacgtt tgccatctgg atgacaaacg 544  
 gaagatccac taaaacgtcc acgggattaa cagaacgtcc ttgcagactg agcgatgaca 604  
 ccacacittg ttiggaacatt taaattcaci ctgcigaata ggaggaagct tttctttttc 664  
 ctggggaaaac aacigictct tggaaatc taccatgaa ctgccttc tagacaactc 724

acatcaaagc cctcacacca ctaatggaga atcctagccc cactaatgcc aagtcctgtt 784  
 ggggatitgt cctcagctat gggcttccct agagtaggtc taggggaata ctcagtciga 844  
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 ctctgacct cgtgatccgc ccgcctcggc ctcccaaagt gctgggatta caggcgtgag 1144  
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 aacgcagatg catagacctt gttcctggta ctgttcagc ctgtgcctgg gagccgigt 1264  
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 aagcacctc agggaaaaag gtgaaaacat tacatccgtg gattctcctg ccacaaccgc 1624  
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 gcaaagtgt gcacactaaa atatcaaatc aaggctgttg gttttaaagt aaatgttttt 1864  
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 cgtgccttct gtcattggga atgaaataaa ttattacgag aaagggactt gtcctaactg 1984  
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 gacagaacta caggagtcat gggaaagaaa attctggctt cactacgtct cactgctcac 2104  
 ttctgatca ctctgatact ttttttttt ttttttttt gcaaccgat accttgaaaa 2164  
 gcttctatgt gtctctcctt ttgttgccg gcagctgtct aggatgatca ctgattacta 2224  
 ttactaagt agccacatgc aaataaaagt tgtttggttaaatgg 2269

<210> 104

<211> 148

<212> PRT

<213> Homo sapiens

<400> 104

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1 5 10 15

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20 25 30

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

35 40 45

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

50 55 60

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65 70 75 80

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

85 90 95

Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

100 105 110

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

115 120 125

Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser

130 135 140

Ile Tyr Tyr His

145

<210> 105

<211> 2899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (2196)

<400> 105

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gggcctcggc tacttggact gcggcggaat atg gcg gct ccg atg act ccc gcg 114

Met Ala Ala Pro Met Thr Pro Ala

1

5

gct cgg ccc gag gac tac gag gcg gcg ctg aat gcc gcc ctg gct gac 162  
Ala Arg Pro Glu Asp Tyr Glu Ala Ala Leu Asn Ala Ala Leu Ala Asp

10

15

20

gtg ccc gaa ctg gcc aga ctg ctg gag atc gac ccg tac ttg aag ccc 210  
Val Pro Glu Leu Ala Arg Leu Leu Glu Ile Asp Pro Tyr Leu Lys Pro

25

30

35

40

tac gcc gtg gac ttc cag cgc agg tat aag cag ttt agc caa att ttg 258  
Tyr Ala Val Asp Phe Gln Arg Arg Tyr Lys Gln Phe Ser Gln Ile Leu

45

50

55

aag aac att gga gaa aat gaa ggt ggt att gat aag ttt tcc aga ggc 306  
Lys Asn Ile Gly Glu Asn Glu Gly Gly Ile Asp Lys Phe Ser Arg Gly

60

65

70

tat gaa tca ttt ggc gtc cac aga tgt gct gat ggt ggt tta tac tcc 354  
Tyr Glu Ser Phe Gly Val His Arg Cys Ala Asp Gly Gly Leu Tyr Ser

75

80

85

aaa gaa tgg gcc ccg gga gca gaa gga gtt ttt ctt act gga gat ttt	402
Lys Glu Trp Ala Pro Gly Ala Glu Gly Val Phe Leu Thr Gly Asp Phe	
90 95 100	
aat ggt tgg aat cca ttt tcg tac cca tac aaa aaa ctg gat tat gga	450
Asn Gly Trp Asn Pro Phe Ser Tyr Pro Tyr Lys Lys Leu Asp Tyr Gly	
105 110 115 120	
aaa tgg gag ctg tat atc cca cca aag cag aat aaa tct gla ctc gtg	498
Lys Trp Glu Leu Tyr Ile Pro Pro Lys Gln Asn Lys Ser Val Leu Val	
125 130 135	
cct cat gga tcc aaa tta aag gta gtt att act agt aaa agc gga gag	546
Pro His Gly Ser Lys Leu Lys Val Val Ile Thr Ser Lys Ser Gly Glu	
140 145 150	
atc ttg tat cgt att tca ccg tgg gca aag tat gtg gtt cgt gaa ggt	594
Ile Leu Tyr Arg Ile Ser Pro Trp Ala Lys Tyr Val Val Arg Glu Gly	
155 160 165	
gat aat gtg aat tat gat tgg ata cac tgg gat cca gaa cac tca tat	642
Asp Asn Val Asn Tyr Asp Trp Ile His Trp Asp Pro Glu His Ser Tyr	
170 175 180	
gag ttt aag cat tcc aga cca aag aag cca cgg agt cta aga att tat	690
Glu Phe Lys His Ser Arg Pro Lys Lys Pro Arg Ser Leu Arg Ile Tyr	
185 190 195 200	
gaa tct cat gtg gga att tct tcc cat gaa gga aaa gta gct tct tat	738
Glu Ser His Val Gly Ile Ser Ser His Glu Gly Lys Val Ala Ser Tyr	
205 210 215	
aaa cat ttt aca tgc aat gta cta cca aga atc aaa ggc ctt gga tac	786
Lys His Phe Thr Cys Asn Val Leu Pro Arg Ile Lys Gly Leu Gly Tyr	
220 225 230	

aac tgc att cag ttg atg gca atc atg gag cat gct tac tat gcc agc	834
Asn Cys Ile Gln Leu Met Ala Ile Met Glu His Ala Tyr Tyr Ala Ser	
235 240 245	
ttt ggt tac caa atc aca agc ttc ttt gca gct tcc agc cgt tat gga	882
Phe Gly Tyr Gln Ile Thr Ser Phe Phe Ala Ala Ser Ser Arg Tyr Gly	
250 255 260	
aca cct gaa gag cta caa gaa ctg gta gac aca gct cat tcc atg ggt	930
Thr Pro Glu Glu Leu Gln Glu Leu Val Asp Thr Ala His Ser Met Gly	
265 270 275 280	
atc ata gtc ctc tta gat gtg gta cac agc cat gct tca aaa aat tca	978
Ile Ile Val Leu Leu Asp Val Val His Ser His Ala Ser Lys Asn Ser	
285 290 295	
gca gat gga ttg aat atg ttt gat ggg aca gat tcc tgt tat ttt cat	1026
Ala Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His	
300 305 310	
tct gga cct aga ggg act cat gat ctt tgg gat agc aga ttg ttt gcc	1074
Ser Gly Pro Arg Gly Thr His Asp Leu Trp Asp Ser Arg Leu Phe Ala	
315 320 325	
tac tcc agc tgg gaa gtt tta aga ttc ctt ctg tca aac ata aga tgg	1122
Tyr Ser Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ile Arg Trp	
330 335 340	
tgg ttg gaa gaa tat cgc ttt gat gga ttt cgt ttt gat ggt gtt acg	1170
Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr	
345 350 355 360	
tcc atg ctt tat cat cac cat gga gtg ggt caa ggt ttc tca ggt gat	1218
Ser Met Leu Tyr His His His Gly Val Gly Gln Gly Phe Ser Gly Asp	

365	370	375	
tac agt gaa tat ttc gga cta caa gta gat gaa gat gcc ttg act tac	1266		
Tyr Ser Glu Tyr Phe Gly Leu Gln Val Asp Glu Asp Ala Leu Thr Tyr			
380	385	390	
ctc atg ttg gca aat cat ttg gtt cac acg ctg tgt ccc gat tct ata	1314		
Leu Met Leu Ala Asn His Leu Val His Thr Leu Cys Pro Asp Ser Ile			
395	400	405	
aca ata gct gag gat gta tca gga atg cca gct ctg tgc tct cca att	1362		
Thr Ile Ala Glu Asp Val Ser Gly Met Pro Ala Leu Cys Ser Pro Ile			
410	415	420	
tcc cag gga ggg ggt ggt ttt gac tat cga cta gcc atg gca att cca	1410		
Ser Gln Gly Gly Gly Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro			
425	430	435	440
gat aag tgg att cag cta ctt aaa gag ttt aaa gat gaa gac tgg aac	1458		
Asp Lys Trp Ile Gln Leu Leu Lys Glu Phe Lys Asp Glu Asp Trp Asn			
445	450	455	
atg ggc gat ata gta tac acg ctc aca aac agg cgc tac ctt gaa aag	1506		
Met Gly Asp Ile Val Tyr Thr Leu Thr Asn Arg Arg Tyr Leu Glu Lys			
460	465	470	
tgc att gct tat gca gag agc cat gat cag gca ttg gtt ggg gat aag	1554		
Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys			
475	480	485	
tcg ctg gca ttt tgg ttg atg gat gcc gaa atg tat aca aac atg agt	1602		
Ser Leu Ala Phe Trp Leu Met Asp Ala Glu Met Tyr Thr Asn Met Ser			
490	495	500	
gtc ctg act cct ttt act cca gtt att gat cgt gga ata cag ctt cat	1650		
Val Leu Thr Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His			



505	510	515	520	
aaa atg att cga ctc att acg cat ggg ctt ggt gga gaa ggc tat ctc	1698			
Lys Met Ile Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu				
525	530	535		
aat ttc atg ggt aat gaa ttt ggg cat cct gaa tgg tta gac ttc cca	1746			
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro				
540	545	550		
aga aaa gga aat aat gag agt tac cat tat gcc agg cgg cag ttt cat	1794			
Arg Lys Gly Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His				
555	560	565		
tta act gac gac gac ctt ctt cgc tac aag ttc cta aat aat ttt gac	1842			
Leu Thr Asp Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp				
570	575	580		
agg gat atg aat aga ttg gaa gaa aga tat ggt tgg ctt gca gct cca	1890			
Arg Asp Met Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro				
585	590	595	600	
cag gcc tac gtg agt gaa aaa cat gaa ggc aat aag atc att gct ttt	1938			
Gln Ala Tyr Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe				
605	610	615		
gaa aga gca ggt ctt ctt ttc att ttc aac ttc cat cca agc aag agc	1986			
Glu Arg Ala Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser				
620	625	630		
tac act gac tac cga gtt gga aca gca ttg cca ggg aaa ttc aaa att	2034			
Tyr Thr Asp Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile				
635	640	645		
gtg cta gat tca gat gca gcg gaa tat gga ggg cat cag aga ctg gac	2082			

Val Leu Asp Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp  
 650 655 660  
 cac agc act gac ttt ttt tct gag gct ttt gaa cat aat ggg cgt ccc 2130  
 His Ser Thr Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro  
 665 670 675 680  
 tat tct ctt ttg gtg tac att cca agc aga gtg gcc ctc atc ctt cag 2178  
 Tyr Ser Leu Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln  
 685 690 695  
 aat gtg gat ctg ccg aat tgaagaggcc tgatttcagc tccaccagat 2226  
 Asn Val Asp Leu Pro Asn  
 700  
 gcagatttgt gttttgtttt ctgttatca ctgtcacaca gcttataaca tgtaigcttt 2286  
 tcagaataca gttgtctagc caagccatca agtgtctgaa attcaatatt ggtttatgca 2346  
 aatacagcaa acttttattt aaglagatag gagaatatgt ttaaaatatt aggaatccta 2406  
 gaccatattt tcaagtcac ttagcagcta ggattctcaa atggaagtgt tataataaat 2466  
 atgtlaaaaa cattttgctt tcttggttaa ttatttgatc cttttaaatc caaatttgaa 2526  
 tcatttgta tgtaigattt tttctgttaa atgtacacag tatttaagat ggatatttgg 2586  
 tggctctatt tgttctgata tcttttggc taaattaaga ggtaccaaga ttgtttcttt 2646  
 gtttcttttt ttcaaattgt gtttagaaat actgtaataa ataigcagta gtgatataaa 2706  
 gaattataac caaggtaata taaaagccat tacgtatgaa ccatccgtg tctcatittg 2766  
 tgttttattt tgtgatcct tgtccactaa gtatcttgtt aaatgccagt atctcagctt 2826  
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<210> 106

<211> 702

<212> PRT



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His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu			
210	215	220	
Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile			
225	230	235	240
Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe			
245	250	255	
Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu			
260	265	270	
Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val			
275	280	285	
His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp			
290	295	300	
Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp			
305	310	315	320
Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg			
325	330	335	
Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp			
340	345	350	
Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly			
355	360	365	
Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln			
370	375	380	
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val			
385	390	395	400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly			

405	410	415	
Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Gly Phe Asp			
420	425	430	
Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys			
435	440	445	
Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu			
450	455	460	
Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His			
465	470	475	480
Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp			
485	490	495	
Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val			
500	505	510	
Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His			
515	520	525	
Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly			
530	535	540	
His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr			
545	550	555	560
His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg			
565	570	575	
Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu			
580	585	590	
Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His			
595	600	605	
Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile			
610	615	620	

Phe	Asn	Phe	His	Pro	Ser	Lys	Ser	Tyr	Thr	Asp	Tyr	Arg	Val	Gly	Thr
625						630						635			640
Ala	Leu	Pro	Gly	Lys	Phe	Lys	Ile	Val	Leu	Asp	Ser	Asp	Ala	Ala	Glu
						645						650			655
Tyr	Gly	Gly	His	Gln	Arg	Leu	Asp	His	Ser	Thr	Asp	Phe	Phe	Ser	Glu
						660						665			670
Ala	Phe	Glu	His	Asn	Gly	Arg	Pro	Tyr	Ser	Leu	Leu	Val	Tyr	Ile	Pro
						675						680			685
Ser	Arg	Val	Ala	Leu	Ile	Leu	Gln	Asn	Val	Asp	Leu	Pro	Asn		
						690						695			700

<210> 107

<211> 790

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78).. (626)

<400> 107

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Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln						
	1		5		10	
aac tac cac	cag gac tca	gag gcc gcc	atc aac cgc	cag atc aac	ctg	158
Asn Tyr His	Gln Asp Ser	Glu Ala Ala	Ile Asn Arg	Gln Ile Asn	Leu	
	15		20		25	
gag ctc tac	gcc tcc tac	gtt tac ctg	tcc atg tct	tac tac ttt	gac	206



gac aag cac acc ctg gga gac agt gat aat gaa agc taagcctcgg 636

Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser

175

180

gctaatitcc ccatagccgt ggggtgacit ccciggtcac caaggcagtg catgcatgtt 696

ggggtttcct ttaccttttc tataagtgt accaaaacat ccacttaagt tctttgattt 756

gtaccattcc ttcaaataaa gaaatttggg accc 790

<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

<400> 108

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln Asn Tyr His Gln Asp

1

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10

15

Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser

20

25

30

Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp Arg Asp Asp Val Ala

35

40

45

Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg

50

55

60

Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn Gln Arg Gly Gly Arg

65

70

75

80

Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys Asp Asp Trp Glu Ser

85

90

95

Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu Glu Lys Asn Val Asn

100

105

110

Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn Asp Pro



115	120	125
His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys		
130	135	140
Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly		
145	150	155
Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe Asp Lys His Thr Leu		
165	170	175
Gly Asp Ser Asp Asn Glu Ser		

180

<210> 109

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<212> DNA

<213> Homo sapiens

<220>

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<222> (256).. (1857)

<400> 109

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gggctgggct gtgcgcctgc gcagtgtagg tcgctcccga ttccctgccc cggccggccc 180
cgccctgggt ccgcaccctc gcccgcctct cagccgccgc tcgccccgc agcagccagc 240
cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291

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Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys

1

5

10

aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339

Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu

15	20	25	
tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag	387		
Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu			
30	35	40	
ttc cac tcg ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg	435		
Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met			
45	50	55	60
gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga	483		
Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg			
65	70	75	
cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggc ccc gag ccc	531		
His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro			
80	85	90	
acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg	579		
Thr Thr Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val			
95	100	105	
gtg ccg ggc aac gcg ctc gtg gtg gac ccg cgg cgc ccc ttc cgc aag	627		
Val Pro Gly Asn Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys			
110	115	120	
ctc aac gcg ttt ggc aac gct ttc ctc aac agg ttc atg tgt gcc cag	675		
Leu Asn Ala Phe Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln			
125	130	135	140
ctg ccc aac ccc gtc ctg gac agc atc agc atc atc gac acc ccc ggg	723		
Leu Pro Asn Pro Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly			
145	150	155	
atc ctg tct gga gag aag cag cgg atc agc aga ggc tat gac ttt gca	771		
Ile Leu Ser Gly Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala			

160	165	170	
gcc gtc ctg gag tgg ttc gcg gag cgt gtg gac cgc atc atc ctg ctc	819		
Ala Val Leu Glu Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu			
175	180	185	
ttc gac gcc cac aag ctg gac atc tcc gat gag ttc tcg gaa gtg atc	867		
Phe Asp Ala His Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile			
190	195	200	
aag gct ctg aag aac cat gag gac aag atc cgc gtg gtg ctg aac aag	915		
Lys Ala Leu Lys Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys			
205	210	215	220
gca gac cag atc gag acg cag cag ctg atg cgg gtg tac ggg gcc ctc	963		
Ala Asp Gln Ile Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu			
225	230	235	
atg tgg tcc ctg ggc aag atc atc aac acc ccc gag gtg gtc agg gtc	1011		
Met Trp Ser Leu Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val			
240	245	250	
tac atc ggc tcc ttc tgg tcc cac ccg ctc ctc atc ccc gac aac cgc	1059		
Tyr Ile Gly Ser Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg			
255	260	265	
aag ctc ttt gag gcc gag gag cag gac ctc ttc aag gac atc cag tca	1107		
Lys Leu Phe Glu Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser			
270	275	280	
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg	1155		
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg			
285	290	295	300
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa	1203		

Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys

305

310

315

gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg 1251

Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val

320

325

330

aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc 1299

Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile

335

340

345

tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag 1347

Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln

350

355

360

acc cag gac ttc agc aag ttc cag gcg ctg aag ccc aag ctg ctg gac 1395

Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp

365

370

375

380

acg gtg gat gac atg ctg gcc aac gac atc gcg cgg ctg atg gtg atg 1443

Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met

385

390

395

gtg cgg cag gag gag tcc ctg atg cct tcc cag gtg gtc aag ggc ggc 1491

Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly

400

405

410

gcc ttt gac ggc acc atg aac ggg ccg ttc ggg cac ggc tac ggc gag 1539

Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu

415

420

425

ggg gcc ggc gag ggc atc cac gac gtg gag tgg gtg gtg ggc aag gac 1587

Gly Ala Gly Glu Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp

430

435

440

aag ccc acc tac gac gag atc ttc tac acg ctg tcc cct gtc aac ggc 1635

Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly  
 445                      450                      455                      460  
 aag atc acg ggc gcc aac gcc aag aag gag atg gtg aag tcc aag ctc 1683  
 Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu  
                          465                      470                      475  
 ccc aac acc gtg cta ggg aag atc tgg aag ctg gcc gac gtg gac aag 1731  
 Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys  
                          480                      485                      490  
 gac ggg ctg ctg gac gac gag gag ttc gcg ctg gcc aac cac ctc atc 1779  
 Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile  
                          495                      500                      505  
 aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac 1827  
 Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His  
                          510                      515                      520  
 ctg gtg ccg ccc tcc aag cgc aga cat gag tgatggcgcc cggccccgca 1877  
 Leu Val Pro Pro Ser Lys Arg Arg His Glu  
 525                      530  
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 ccgtcactcc atacagtatt aggtgaggat ggaatcgggc gctgtccttg ccgggaagtc 3377  
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<210> 110

<211> 534

<212> PRT

<213> Homo sapiens

<400> 110

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys Lys Glu Pro Glu

1

5

10

15

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20	25	30	
Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His Ser Pro			
35	40	45	
Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val			
50	55	60	
Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu			
65	70	75	80
Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser			
85	90	95	
Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn			
100	105	110	
Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe			
115	120	125	
Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro			
130	135	140	
Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly			
145	150	155	160
Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu			
165	170	175	
Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His			
180	185	190	
Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys			
195	200	205	
Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile			
210	215	220	
Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu			
225	230	235	240

Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser			
	245	250	255
Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu			
	260	265	270
Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn			
	275	280	285
Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala			
	290	295	300
Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn			
305	310	315	320
Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly			
	325	330	335
Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp			
	340	345	350
Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe			
	355	360	365
Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp			
	370	375	380
Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu			
385	390	395	400
Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly			
	405	410	415
Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu			
	420	425	430
Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr			
	435	440	445



Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly  
 450 455 460  
 Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val  
 465 470 475 480  
 Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu  
 485 490 495  
 Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu  
 500 505 510  
 Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro  
 515 520 525  
 Ser Lys Arg Arg His Glu  
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<210> 111

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89).. (724)

<400> 111

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Met Gly Glu Ile Lys Val Ser Pro

1

5

gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg 160

Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val

10	15	20	
gat gat gat gac agt aag ata tgg tgc ctc tat gac gcg ggc ccc cga			208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg			
25	30	35	40
agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca			256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala			
45	50	55	
gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg			304
Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg			
60	65	70	
gtt atc gct ttg cag tat cca gtt tat tgg gac cat ctc gag ttc tgt			352
Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys			
75	80	85	
gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat			400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His			
90	95	100	
ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa			448
Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu			
105	110	115	120
tac act cac aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc			496
Tyr Thr His Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser			
125	130	135	
ttc agt gac acc tct atc ttc aac caa act tgg act gca aac agc ttt			544
Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe			
140	145	150	
tgg ctg atg cct gca ttt atg ctc aaa aaa ata gtt ctt gga aat ttt			592
Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe			

155	160	165	
tca tct ggc ccg gtg gac cct atg atg gct gat gcc att gat ttc atg	640		
Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met			
170	175	180	
gta gac agg cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt	688		
Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu			
185	190	195	200
acc ttg aaa ttg tca aaa ttc tta tgt gga acc tca taaaattcgg	734		
Thr Leu Lys Leu Ser Lys Phe Leu Cys Gly Thr Ser			
205	210		
ggacatacct gtaactattta tggatgtgtt tgaicagagt gcgcattcaa ctgaagctaa	794		
agaagaaaatg tacaagctgt atccctaattg ccccgaagag gctcatctga aaacaggagg	854		
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kgcaattccw kggrrggaccm aatagcggc ctttgaccca tcaatggta gtgccgagga	974		
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<210> 112

<211> 212

<212> PRT

<213> Homo sapiens

<400> 112

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1 5 10 15

Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp

20 25 30

Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe

35 40 45

Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu

50 55 60

Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val

65 70 75 80

Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp

85 90 95

His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly

100 105 110

Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val

115 120 125

His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn

130 135 140

Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu

145 150 155 160

Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met

165 170 175

Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly  
180 185 190  
Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Lys Leu Ser Lys Phe Leu  
195 200 205  
Cys Gly Thr Ser  
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<210> 113

<211> 2391

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (360)

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<222> (49)

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<222> (51)

<223> a or t

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<222> (54)

<223> t or c

<220>

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<223> g or t

<220>

<221> unsure

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<221> unsure

<222> (1705)

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<400> 113

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Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys	
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kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa	96
Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys	
20 25 30	
gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac	144
Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His	
35 40 45	
cga gag acc tcc atg gtc cat gaa ctg aac cgg tac atc ccc aca gcc	192
Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala	
50 55 60	
gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctg tgc gtc ctg gct gac	240

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp  
65 70 75 80  
ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca 288  
Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr  
85 90 95  
atc atc tac cag tac ttt gag atc ttc gtt aag gag yaa agc gag gtt 336  
Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val  
100 105 110  
ggc agc atg ggg gcc ctg ctc ttc tgagcccgtc tcccggacag gttgaggaag 390  
Gly Ser Met Gly Ala Leu Leu Phe  
115 120  
ctgctccaga agcgccctcg aaggggagct ctcakcatgg cgcgtgctgc tgcggcatai 450  
ggacttttaa taatgtgttt tgaatttcgt attctttcat tccactgtgt aaagtgttag 510  
acatlltcca attlaaaatt ttgctlltta tccitggcact ggcaaaaaga actgtgaaag 570  
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<210> 114

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (17)

<223> unknown

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<221> unsure

<222> (109)

<223> unknown

<400> 114

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1

5

10

15

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp

65	70	75	80
Phe	Leu	Gly	Ala
Ile	Gly	Ser	Gly
Thr	Gly	Ile	Leu
Leu	Ala	Val	Thr
85	90	95	
Ile	Ile	Tyr	Gln
Tyr	Phe	Glu	Ile
Phe	Val	Lys	Glu
Xaa	Ser	Glu	Val
100	105	110	
Gly	Ser	Met	Gly
Ala	Leu	Leu	Phe
115	120		

<210> 115

<211> 599

<212> DNA

<213> Homo sapiens

<400> 115

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agttaggctg gagggagtta aggtcagiat ggaagatagg gttaggacag ggtgctttgg 180
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atgagaaggt gctcttactic agttaatgat gagtgactat atttacaaa gcccctacct 300
gctgctgggt cccttgiagc acaggagact tgggctaagg gcccctccca gggaaggagac 360
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gaggactagc aggaggcagc cttagagaaac cggcagttcc caaagccagc gcctggctgt 480
tctctcattg tcactgccct ctccccaacc tctctcttaa cccactagag attgcctgtg 540
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<210> 116

<211> 364

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (134)

<223> a, c, g or t

<220>

<221> unsure

<222> (135)

<223> a, c, g or t

<220>

<221> unsure

<222> (179)

<223> g or a

<400> 116

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cacagttcca ggannggta ggtagcagtg tgtgtgttat gtgccactga cctgaaara 180

tgtgccatag cccaagccaa ttgaaatiga tcagggggcc aggcatggtg gctcatgcct 240

gtaatcccag caccttggga agctgaggtg ggaggattgc ttgaaaccag gagttcaaga 300

ccagcctgtg caacatagca aaaccccatc tctacaaaga ttaaaaataa aaaattagct 360

&lt;210&gt; 117

&lt;211&gt; 852

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (26).. (217)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (37)

&lt;223&gt; a, c, g or t

&lt;400&gt; 117

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                               Met Asp Gly Xaa Val Thr Phe Leu Thr
                               1             5
agc tgg gct aac ctt tcc cga act tgt ttc ccg gag gca agg tgc tcg   100
Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser
   10             15             20             25
gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tcg agg cta ggg   148
Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly
           30             35             40
cat tac gtt tcg tgg aac caa agc agc caa ttg cat agc aag tat ttt   196
His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe
           45             50             55
cct gca ttc caa tta aat gct taagaaaaag cagcaltccta taaaattgtg   247

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Pro Ala Phe Gln Leu Asn Ala

60

atcataaaca tccatttccc tcagcttttg tgagtgccct gacttacagc caacatcact 307  
gtttaactca gtcgttttaa aaacaaactt ttcgtgtggt tgataacaga gagttgctcc 367  
ctgagccatc agggctcctgg gagctggaag tgaagggtt attaacattc tacctttatg 427  
cagctgttgg ctgaccagaa taaactccct gctgagttca agctttgaat ggaatggatg 487  
caaatgatgt tgtttccatt agagcaggig ctacacagcat tctgattggc ctgagcagac 547  
cgaggctatg gctgttggga caagcttagc atcctggaca tcttgtcaaa gaacctcact 607  
caccctctg gcctctacag ccctcagagg agagaaaacc aattctccaa caaacaggic 667  
tctccaacat ggtggtgctg gcaggcttag gtttagaaaa tctgactgt taaaggcgtt 727  
tgaatacatc acattcciat gcaaagtgtt ttaatctcca gtttaatgia gtttatitit 787  
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<210> 118

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (4)

<223> unknown

<400> 118

Met Asp Gly Xaa Val Thr Phe Leu Thr Ser Trp Ala Asn Leu Ser Arg

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5

10

15

Thr Cys Phe Pro Glu Ala Arg Cys Ser Val Thr Gln Arg Ile Leu Thr

20

25

30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

35

40

45

Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

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<210> 119

<211> 1156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (524).. (1105)

<220>

<221> unsure

<222> (10)

<223> a or t

<400> 119

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gctagagaca gggagagcag agtaaaaccc tcaggctgct gaaatttcta ggctgttagg 180  
aagcccctcg aattcigtga aaatgagggt ttcttaactc acacigagag cggaagggg 240  
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aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagaggga 480  
actgacagca gctgcggctg cagggggcaa cgacgagaag aag atg ttg aag tgt 535

Met Leu Lys Cys

gtg gtg gtg ggg gac ggt gcc gtg ggg aaa acc tgc ctg ctg atg agc 583  
 Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Met Ser  
 5 10 15 20  
 tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc act gtg ttt gac 631  
 Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro Thr Val Phe Asp  
 25 30 35  
 cac tat gca gtt act gtg act gtg gga ggc aag caa cac ttg ctc gga 679  
 His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln His Leu Leu Gly  
 40 45 50  
 ctg tat gac acc gcg gga cag gag gac tac aac cag ctg agg cca ctc 727  
 Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln Leu Arg Pro Leu  
 55 60 65  
 tcc tac ccc aac acg gat gtg ttt ttg atc tgc ttc tct gtc gta aac 775  
 Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn  
 70 75 80  
 cct gcc tct tac cac aat gtc cag gag gaa tgg gtc ccc gag ctc aag 823  
 Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val Pro Glu Leu Lys  
 85 90 95 100  
 gac tgc atg cct cac gtg cct tat gtc ctc ata ggg acc cag att gat 871  
 Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly Thr Gln Ile Asp  
 105 110 115  
 ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg tat atg aaa gag 919  
 Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu Tyr Met Lys Glu  
 120 125 130  
 aaa cct ctc act tac gag cat ggt gtg aag ctc gca aaa gcg atc gga 967  
 Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala Lys Ala Ile Gly



135	140	145	
gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa			1015
Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys			
150	155	160	
gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag			1063
Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys Lys			
165	170	175	180
aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc			1105
Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile			
185	190		
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<210> 120

<211> 194

<212> PRT

<213> Homo sapiens

<400> 120

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Leu	Leu	Met	Ser	Tyr	Ala	Asn	Asp	Ala	Phe	Pro	Glu	Glu	Tyr	Val	Pro
				20						25					30
Thr	Val	Phe	Asp	His	Tyr	Ala	Val	Thr	Val	Thr	Val	Gly	Gly	Lys	Gln
				35						40					45
His	Leu	Leu	Gly	Leu	Tyr	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asn	Gln
				50						55					60
Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asn	Thr	Asp	Val	Phe	Leu	Ile	Cys	Phe
65										70					75
															80

Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val  
                     85                    90                    95  
 Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly  
                     100                    105                    110  
 Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu  
                     115                    120                    125  
 Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala  
                     130                    135                    140  
 Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln  
 145                    150                    155                    160  
 Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His  
                     165                    170                    175  
 Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser  
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<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (259)

<220>

<221> unsure

<222> (28)

<223> a, c, g or t

<220>

<221> unsure

<222> (388)

<223> g or a

<220>

<221> unsure

<222> (631)

<223> a or t

<220>

<221> unsure

<222> (637)

<223> g or a

<220>

<221> unsure

<222> (638)

<223> g or a

<220>

<221> unsure

<222> (639)

<223> g or a

<400> 121

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Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

acc gtg tat gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc 97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20	25	30	
ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac	145		
Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn			
35	40	45	
atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg	193		
Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala			
50	55	60	
ctg gct gtg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act	241		
Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr			
65	70	75	80
gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc	289		
Val Lys Val Trp Thr Cys			
85			
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<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<223> unknown

<400> 122

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1 5 10 15

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20 25 30

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

35 40 45

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

50

55

60

Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

65

70

75

80

Val Lys Val Trp Thr Cys

85

<210> 123

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (168).. (350)

<220>

<221> unsure

<222> (343)

<223> g or a

<220>

<221> unsure

<222> (422)

<223> t or c

<220>

<221> unsure

<222> (457)

<223> g or c

<400> 123

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gccaaacttg gtigaagact aggtcttccc tggcaagtgc cggaaga atg gac tta 176

Met Asp Leu

1

ctg act ttt atc aac tct tct cac tgc caa ggc caa cag cat ctg agg 224  
Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln His Leu Arg

5

10

15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt 272  
Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20

25

30

35

ctg tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt 320  
Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

40

45

50

gct tca gag cct ttg cag ctg cra cct agt tgaatccaca taggsttcct 370  
Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

55

60

tccacacggt gggaaggatc ttgctgcttt cactcacagg accagggagt tyttcaatca 430  
ggagggtgggt ttttgttccc ttcaggscit tggcaacatc tagagacagt ttgtattgcc 490  
acgcctggag tgggatgtgt gtgctacttg catctagtgg ctgctaaaca tccctacactg 550  
cataggatag tccccactac cccagccaa gaattatctg atccagggg tca 603

<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (59)

<223> unknown

<400> 124

Met Asp Leu Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln

1 5 10 15

His Leu Arg Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly

20 25 30

Gly Tyr Phe Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr

35 40 45

His Cys Cys Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

50 55 60

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775).. (1017)

<220>

<221> unsure

<222> (200)

<223> g or a

<400> 125

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ttttccctga ctccagcagg gcaaggaatg taaccgagag gtigtgtggg ctgggctctg 180  
 gtgccctctt ccttgcccr gaacacctct cctcctgatt ccttggcac ctigtcttct 240  
 tgtctgttta cctgtctccc tgcctgceca tctgcatctt ttgcagccca ctctgacttc 300  
 catctggggg ctgagaccac ccttgccctgc ccccttcttt ctgccctaag aatgtccttt 360  
 taggctgggc atggttgtca cgcctgtaac ccagcactt tgggaggcgg agacgggcag 420  
 ataacctgag gtcaggattt cgagaccaac ctgacctaca tggagaaact ccgcctctag 480  
 taaaaataca aaattagccg ggcatgggtg tgcacgcctc taatcccagc tactcgggag 540  
 gctgaggcag gagaatcact tgaacccggg aagtggaggt tgcagtgagc caagagtaca 600  
 ccactgcact ccagccctggg caacagagcg agactccgtc ttaaaaaaaaa aaaaaaaaaag 660  
 aacgcccttt tactgtcttc atcatcccag tttagggcag tgctggagtg gggaaggccg 720  
 tcttagacca tagaggttgg aagacgtga gagatcatcc agcccagccc ctg atg 777

Met

1

tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac 825  
 Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His  
 5 10 15  
 ggt cat acg gca ggt tgc cac aaa acc aag atg gca gcc ctt cct cag 873  
 Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln  
 20 25 30  
 cgt gcc tca ctg cca ctg cca gag cca ggg agc ccc ata aaa ccc aca 921  
 Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr  
 35 40 45  
 tca tgt ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg 969  
 Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp  
 50 55 60 65  
 gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga 1017

Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly

70

75

80

tgacagacag ctigcccgca cactcgggcc ccactcaagg atgtagggcc tttctiggcc 1077

cctgaccctt ccttgggcat tgggagcgtg gggacggggc tggccttggg aggagcggca 1137

ggggcatcac ctcttctgc tgccttctcc tgcctctacc ctcaagggcc tgggggctgc 1197

ccagctgcct ctatgccctt ctgggggtct cagccactg ctgacacttc tgcaatccag 1257

agaaacacia aataaagcaa tacgtgtttg cc 1289

<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

<400> 126

Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala

1

5

10

15

His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro

20

25

30

Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro

35

40

45

Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro

50

55

60

Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu

65

70

75

80

Gly

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734).. (886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

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aagttgatgg caattcttca catgtaaaca gtgccagtgc acagaacctt tatataattt 360
tgaagccag tactgtgctc tgcatataac aaagctgctt caaggatgag acctttttct 420
aaaagcatgt aatgtgagaa gccggcctgc cttattttct tttttctttt ttaatgatta 480
aaaatagttt gtggcaaggc acggtggctc aggcctgtaa ttctagcact ttgggaggcc 540
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actgcatctc tacagagagt aaaaaaaaaatt acccgagtgt ggtgatgtgc atctgtaatc 660
tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720
gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga 769
```

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

1

5

10

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ccc tgt ctg aaa aaa aaa aat ata tat ata tat ata tat tat ttt 817
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Pro Cys Leu Lys Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe  
15 20 25  
tat gag gtg aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga 865  
Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly  
30 35 40  
acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt 916  
Thr Ser Trp Lys Thr Thr Pro  
45 50  
gattcctgct ttcagaagga ggtggattca aatacatcaa aagtccttc ctctgctaag 976  
tgtttatagt tcaatgaata atttcaatat ttgtatgtgt tcttgtcatt ttattttttt 1036  
ctgaaaaact tccaaaaatt tgaaaataaa attacagcct tttcttctt 1085

<210> 128

<211> 51

<212> PRT

<213> Homo sapiens

<400> 128

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys  
1 5 10 15  
Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys  
20 25 30  
Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys  
35 40 45  
Thr Thr Pro  
50

<210> 129

<211> 1544

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

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acaaaaaccc aattttgttc atattgaagc atgaaataaa tgagagcaag giagggccaa 180

attaactctt gtggacagtc cctaaaagtc cagttctaca ttgttgaaaa ttgtggtgcc 240

atgaattaag atggatgact ggaaaaaggt gtggagaaa gagttaaaga tgaggaagag 300

atatTTTTtag tataatgaagt tatccaggga ctgatattc ataattcagt gctgtggaaa 360

tgaaaaaaat gattgaagag gtggaacgga aatgacctta gggggaaaaa aaaggaccaa 420

agaagtccta ttaaaagttg aaatcagtat ttctgaattc aaattgcttg aatttccaaa 480

atagtcagta aaggatctaa tagaaccaga attatttggg tgaattctgc aggttttatg 540

ggcttgtcac aacgtgaagg gctggaatgt atattaccaa atgggaattt ccatgtagg 600

tttttgctag tcccaccccc attttagcct aatttggctt aaacgcagta tggggagaat	660
tgttcccat tccatgtgtc tgaattcagc tcatctccca gcatatagat atatccicct	720
ttaactccga ccagaacct tcttccgtg gcactcccca cccatagacc ttcagatcat	780
ctccacacc ctggatctca ctctcctctt agtaacagag acactcctga ggttggactt	840
ccttgccttt ctctacttcc aaatcacaat ttcttacaac caagctttgt gctcccgagt	900
aagcagggat gtactagggg aatgtaaaac tgcaaaccta aaaacctgca tcttcttgaa	960
gcatcagttt tacttaccaa atggtttaga gtcataagat gacctatitt tatataaaag	1020
ttatattata gaataaaatg ttcatatgca tagactgita agataaaaaa ataggraatc	1080
tigcaaggta attcttattt gcaagtgggt tatgtgttca ctctcctcta cctttatggt	1140
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cigttaaccc agggcctaga ctcttagtgc ctctgaggca gaaccaaagg agcctgcact	1260
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ttaggaccag ctgattgita tgcctgcagg atggtttga aacagaaaca atacttgttt	1380

actgtaggaa tcciatittat attatitttc agtcctgtga atgctgtgaa aagatttatt 1440

ccittgaggc caggaagctc ccaggcaiat atgcttctag gtiaggattg tcttgactca 1500

ctaaagatgc caggatatig gggctgaggg gagtttgagg tgtt 1544

<210> 130

<211> 508

<212> DNA

<213> Homo sapiens

<400> 130

tgaaatcagg gctggagctt tacttaggat tcacatggcc tcttaggaac catgggacaa 60

atgggaaaca ggttatcggg ggattcatga agtcagttag agtaattgct tcttttttgc 120

gggtgaactg aatgtatttc ttacacaaat cttagatgta acaattaaaa agaagaaatg 180

acatgcaagt aggtcttagc agaaaaatgc aggctgggca tgagtcatgt gtllaccctc 240

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttcttgaagt tattgttagt 300

atttggtaic tcaaattttt cgtcactgtt cacatgccac ttctctctgtg cacagtggta 360

tcttcatttg ctttttaacc tacactgagg agtctttgtc aggttgcact gattttccaa 420

ttctgcagta atgagtaagc tcacggcatg gggaagaaga cagtcagtc aatgaagttc 480

tctaaattat tttaacattg cctttgaa

508

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)

<223> g or t

<220>

<221> unsure

<222> (54)

<223> g or c

<220>

<221> unsure

<222> (300)

<223> g or c

<220>

<221> unsure

<222> (407)

<223> g or a

<220>

<221> unsure

<222> (415)



<223> a, c, g or t

<220>

<221> unsure

<222> (417)

<223> g or c

<220>

<221> unsure

<222> (419)

<223> t or c

<220>

<221> unsure

<222> (430)

<223> a or t

<220>

<221> unsure

<222> (448)

<223> t or c

<220>

<221> unsure

<222> (449)

<223> g or t

<220>

<221> unsure

<222> (472)

<223> a, c, g or t

<400> 131

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gtggccaccc ttgggctcag acagctcigg gccttttgac cacaagccag cccctcgccc	180
tcctcgtggc atagcttctt ctgcccagg actgcagggc ggcttcctcc aaggcttcca	240
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cacgtatggw gcaggttgtc ctggtccykg ggtgcaggga agtgggctgc anggaagtgg	480
attggagggg agcttgagga atataaggag cgggggtgga gactcaggct atggacaagg	540
acagcccca ggttgggaag acctggcctt agtcgtcctc agcctagggg cagggcagt	600
aagaaagctc tccccgtcc tgctgtaatg acccagagta gccctcccag gccggcatct	660
tatgtgtgtc tccaccaic ctcatggtgg cacitttcta ggctgtctc ccagcatgt	720
gcaaggctcg gaagagaacc agggaagtga aacitgggta aaacagaaag ctcaatggat	780

gggctagggt cccagatca ttagggcaga gttgcacgt cctctggica ctggaatcca	840
cccagcccac gaatcatctc cctcttgaag gatititatt ctactgggtt ttggaacaaa	900
ctcctgctga gacccacag ccagaaactg aaagcagcag ctcccaaag cctggaaaat	960
ccctaagaga aggcctgggg caggaagtg agtgacagg gacaggtaga gagaaggggg	1020
cccaatggcc agggagtga ggaggiggcg ttgctgagag cagictgcac atgcitctgt	1080
ctgagtgcag gaaggtgttc cagggtcgaa attacattc tcgtacctgg agacgctgtt	1140
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cctg	1204

<210> 132

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (223)

<223> a, c, g or t

<220>

<221> unsure

<222> (237)

<223> a, c, g or t

<220>

<221> unsure

<222> (380)

<223> a, c, g or t

<220>

<221> unsure

<222> (468)

<223> a, c, g or t

<400> 132

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acactccagc ctgggtgaca gattgagatc ctgtctcaaa aaaagagaaa gaaaaccttt 120

gagattcttc cattttttaga gctgagagag cacttgtgaa acacacacac atgcacaaac 180

atataaacat gcatacaggc atgcacatgc acacacaaat acncatacac acacacnagc 240

acacacacac caccaccacc atcatcagag gaacttacag aaaaggggac atttatagat 300

tcctaggaat atgccaaagc ttttcaaagc ctctatggac agctcattcc ttaacttttc 360

ctcttttaaaa tctttttttan cttcttattt gccccagcca ctatcacatgc ctgaggcagc 420

tgcaacgtta aacaattgcc actgattact ttcaacaaat aacctcanag aaaaggctgt 480

gtgtattgaa tgggtatcaa gtcacgtc

508

<210> 133

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (313)

<223> a, c, g or t

<220>

<221> unsure

<222> (336)

<223> g or c

<220>

<221> unsure

<222> (401)

<223> g or c

<400> 133

gtcgactcga gcggccgcgg accgtttttt ttttttttct ctccctcigcc ctttctaata 60

tcttggagag ggatggagac tgaagagtga gtttggtcct ccacttgatc caggttctta 120

tttttgtttt ctacttcaaa gcgagaactt ggtactgiga ctltgataag aattgacttc 180

aggcccagca agatccctca tgccctgtaat cccagcacit tggggggcca aggcaggagg 240

attgcgtgag cccaggagtt cgagacccac ctgggcaaca tagggacctt gtctctacaa	300
aaaataaaat tancigggtt tgatggigca catcastggt cctggctact cgggaggcca	360
aggtagggagg aatgcttgag gatcggaggt caaggctgca sigagccaat attgtgccac	420
tgcatccag cctgggcaac agagtggagac actgtcttaa aaaaaaaaaa aaaaaacggt	480
ccgc	484

<210> 134

<211> 605

<212> DNA

<213> Homo sapiens

<400> 134

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tacacagcat ttttaacacc tttttttctt agtttttttg ttcggttttg ttttccatca	120
ggaatttgag ttctctctaa cccagcttac tgtgggacat aggaaaactc agtagaaata	180
ccittgggtga tcttggtgag ttttaagtcg atcttgaict taaactcagt aagccactat	240
ctgcaatttt gtacattata tagtattttg aagataigga accttatgaa aaaaaaatag	300
caaattagtt ctttttcccc cagaggggaa agttaatgic tgcaaatagt gtgtgtctta	360

ttttactgtt gaacagcaat tgctatttat ttttttatig cctagaactt caacaigtg	420
tataggaatc ctgtagtgcc actagttaaa tgccgaattc tcatctggat gtiaccatca	480
aacalcagta cactigtcat ttcacatgtg tttaatgtga cagttttica gtactgtatg	540
tgtaaatttc tacttttttt aatatitaaa attgctttta aataaacata ttctcagtig	600
atccc	605

<210> 135  
 <211> 1786  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (2).. (151)  
 <220>  
 <221> unsure  
 <222> (689)  
 <223> g or a  
 <400> 135

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 Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1	5	10	15
---	---	----	----

tac ctc tct cca cag cag ggc tct caa aac cat ttt gat ccc cca ttg 97  
 Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu  
 20 25 30  
 gca gag ggt tcc cct ctt tac aga gtt cag tca tta aaa gca tgg atc 145  
 Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile  
 35 40 45  
 agc tgt taatctcatt ggaggagga actgtttcct gcattcattc atctgggaac 201  
 Ser Cys  
 50  
 ctcttgagt agccactgtc tgccagccac tgctctagag atgggaaaac agcacggaac 261  
 aaaaccaagg tctttcttcc agcgaattta tctcttcag gaagctgggt cctgccacca 321  
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 acggaagaat gggcctgggg cagaacaaat agggagcatt tgaaagcttc tggctgataa 681  
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 aatggtagca tcttttccat aactcagctt cttttccctt gtttccctga agtgtgacgt 1041  
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<213> Homo sapiens

<220>

<221> CDS

<222> (535).. (729)

<400> 137

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agtlactaaa atttacacat cttaaaagtg tgtaaatgct taaatttcag aattaccatc 120  
agaaccicaa ttgacattcc ttigaaatagg ctaataagtg acaaataaga ttaataagat 180  
ttttcaaaat cgccaggact ggtgaatata aatgatgatt gaaciggaat aatattgggg 240  
accaaataca atgaatgatt aaattatgaa gctcatalcc ttttgaaggt agttgcaaag 300  
agacatttca aaactgccct aggccattgc agcatcctta gatgggacgc ataataatta 360  
ccttaaagca tcaccactca ttttgacatc atagatttta ttatgttagt ttaaaaggtc 420  
aatcagccic atgactttat agttaatgct tgtattttaa aacatititit atacatttgg 480  
ttaigttagt aaaccaaaaa catttgattt ataaaatatc tatttgaata aatt atg 537

Met

1

agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585  
Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr

5

10

15

aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633  
Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr

20

25

30

tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681  
Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu

35

40

45

aga ttt tcc att aac tat ttt ttt caa aga ctc aaa ttt tgt acc aag 729

Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys  
 50 55 60 65  
 taaatccagg ctttatgtac aaacatgttg ttgttttat ttggggctgg gggaggtata 789  
 tgaatgagcag acttctcgga attcataata aattttctaa aagcct 835

<210> 138

<211> 65

<212> PRT

<213> Homo sapiens

<400> 138

Met Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile  
 1 5 10 15  
 Tyr Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met  
 20 25 30  
 Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu  
 35 40 45  
 Leu Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr  
 50 55 60  
 Lys  
 65

<210> 139

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (201)

<220>

<221> unsure

<222> (348)

<223> t or c

<220>

<221> unsure

<222> (353)

<223> a or t

<220>

<221> unsure

<222> (358)

<223> a or t

<220>

<221> unsure

<222> (363)

<223> a or t

<220>

<221> unsure

<222> (368)

<223> g or a

<400> 139

tgt ttc agt gtg act gtc ttg tta gag gtg aag ttt atc cag ggt aac 48

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1

5

10

15

ttg ctc act aac tat tcc ttt tta tgg cct ggg gtt aaa ggg agc atg 96

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met  
 20 25 30  
 gct cac act ggt gaa aat aag gaa ggc ctg gtc tta tct tgt att aat 144  
 Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn  
 35 40 45  
 aat act ggc tgc att cca cca gcc aga gat ttc tat ctg cga aga cct 192  
 Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro  
 50 55 60  
 atg aaa cac tgaagagaaa tgtaggcaga aggaaatggc cacatatcac 241  
 Met Lys His  
 65  
 aagttctatt atatatcttt ttgtaaatac atattgtata ttacttggat gttttcttat 301  
 atcatttact gtctttttga gttaatgica gtttttactc tctcaaytta cwatgtwaca 361  
 twglaartaa cataatgtcc tttattatit atatttaagc atctaacata tagagttggt 421  
 ttcatataag tttaagataa atgtcaaaaa tataatgttct ttgtttttc ttgtctttaa 481  
 aattatgtat cttttccttt tctttttttt aagaataatt tattgttcag gagaaagaat 541  
 gtatatgtaa ctgaaactat ctgaagaatg cacattgaag gccgtgaggt actgataaac 601  
 taaagaatit attattcaaa atact 626

<210> 140

<211> 67

<212> PRT

<213> Homo sapiens

<400> 140

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn  
 1 5 10 15  
 Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

	20		25		30										
Ala	His	Thr	Gly	Glu	Asn	Lys	Glu	Gly	Leu	Val	Leu	Ser	Cys	Ile	Asn
	35		40		45										
Asn	Thr	Gly	Cys	Ile	Pro	Pro	Ala	Arg	Asp	Phe	Tyr	Leu	Arg	Arg	Pro
	50		55		60										
Met	Lys	His													
	65														

<210> 141

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103).. (525)

<400> 141

aagaaatgga ggaticagaa ccaaggattt ccaagtgatt tcttccaaag cacaggaatc 60

tcactctgtt aaagctggtc tgttctaaact gagaigacag tc atg tcc ctt tcc 114

Met Ser Leu Ser

1

agg gac ctc aag gac gac ttt cac agt gac acg gta ctc tcc atc tta 162

Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val Leu Ser Ile Leu

5	10	15	20
---	----	----	----

aat gag cag cgc att cgg ggc att tta tgc gat gtc act atc att gtg 210

Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val Thr Ile Ile Val

25	30	35
----	----	----

gaa gat acc aaa ttt aaa gcc cat agc aat gtt ctg gca gct tca agc 258

Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser	
40	45
50	
ctg tat ttt aaa aat atc ttt tgg agc cat aca atc tgt att tcc agc	306
Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser	
55	60
65	
cac gtc ctg gag ctg gac gat ctc aaa gct gaa gtg ttt act gaa ata	354
His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile	
70	75
80	
ctt aat tat atc tac agt tcc aca gtc gtt gtc aag aga cag gaa aca	402
Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys Arg Gln Glu Thr	
85	90
95	100
gtc act gat ctc gca gct gca gga aaa aag ctg gga ata tcg ttc ttg	450
Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly Ile Ser Phe Leu	
105	110
115	
gaa gac ctt act gat cgc aac ttc tca aat tcc ccg ggt ccc tat gta	498
Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro Gly Pro Tyr Val	
120	125
130	
ttc tgt att act gaa aag gga gtg gtt	525
Phe Cys Ile Thr Glu Lys Gly Val Val	
135	140

<210> 142

<211> 141

<212> PRT

<213> Homo sapiens

<400> 142

Met Ser Leu Ser Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val

1	5	10	15
Leu Ser Ile	Leu Asn Glu Gln Arg Ile Arg Gly Ile	Leu Cys Asp Val	
20	25	30	
Thr Ile Ile	Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val	Leu	
35	40	45	
Ala Ala Ser Ser	Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr	Ile	
50	55	60	
Cys Ile Ser Ser	His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu	Val	
65	70	75	80
Phe Thr Glu Ile	Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val	Lys	
85	90	95	
Arg Gln Glu Thr	Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu	Gly	
100	105	110	
Ile Ser Phe Leu	Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser	Pro	
115	120	125	
Gly Pro Tyr Val	Phe Cys Ile Thr Glu Lys Gly Val Val		
130	135	140	

<210> 143

<211> 1827

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138).. (1307)

<400> 143

gagacttggg ctggagccgc cctgggtgtc agcggctcgg ctcccgcgca cgctccggcc 60



gtcgcgacgc ctcggcacct gcaggiccgt gcgtcccgcg gctggcgccc ctgactccgt 120  
 cccggccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac 170  
 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn  
 1 5 10  
 ttg ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc tgc 218  
 Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser  
 15 20 25  
 cgg gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg 266  
 Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val  
 30 35 40  
 gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag 314  
 Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu  
 45 50 55  
 gtg tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc 362  
 Val Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe  
 60 65 70 75  
 aaa cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc 410  
 Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val  
 80 85 90  
 aca aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg 458  
 Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg  
 95 100 105  
 aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc 506  
 Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro  
 110 115 120  
 tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc 554  
 Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly

125	130	135	
cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct			602
His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro			
140	145	150	155
cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc			650
Pro Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr			
160	165	170	
ctg agc tgc cag tct cca agg agt aag cct gct gtc caa tac cag tgg			698
Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp			
175	180	185	
gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat			746
Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp			
190	195	200	
gtc atc cgt ggg tct tta agc ctc acc aac ctt tcg tct tcc atg gct			794
Val Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala			
205	210	215	
gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt			842
Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys			
220	225	230	235
aat gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct			890
Asn Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala			
240	245	250	
gga gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg			938
Gly Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu			
255	260	265	
gtc ctc ttg tac cac cgc cgg ggc aag gcc ctg gag gag cca gcc aat			986

Val Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn  
270 275 280  
gat atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag 1034  
Asp Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys  
285 290 295  
agc tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc 1082  
Ser Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser  
300 305 310 315  
gca cga gcc ctc tgg cca ccc cat ggc cct ccc agg cct ggt gca ttg 1130  
Ala Arg Ala Leu Trp Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu  
320 325 330  
acc ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg 1178  
Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu  
335 340 345  
ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt 1226  
Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly  
350 355 360  
ggg gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg 1274  
Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met  
365 370 375  
gtg cct gcc cag agt caa gct ggc tct ctg gta tgaatgacccc accactcatt 1327  
Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val  
380 385 390  
ggctaaagga ttggggctc ctcttccta taagggtcac ctctagcaca gaggcctgag 1387  
tcatgggaaa gattcacact cctgaccctt agtactctgc cccaccctct ctttactgig 1447  
ggaaaacat ctcatgaaga cctaagtgic caggagacag aaggagaaga ggaagtggat 1507  
ctggaattgg gaggagcctc caccacccc tgactccccc ttaatgaagcc agctgctgaa 1567

attagctact caccaagagt gaggggcaga gatttccagt cactgagtct cccaggcccc 1627  
 ctatgatctgt accccacccc tatctaacac cacccttggc tcccactcca gctccctgta 1687  
 ttgatataac ctgtcaggct ggcttggtaa ggttttactg gggcagagga tagggaatct 1747  
 cttattaaaa ctaacatgaa ataigtgttg ttttcatttg caaatitaaa taaagataca 1807  
 taatgtttgt atgagataag 1827

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1 5 10 15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln

20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val

35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	
Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile			
290	295	300	
Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp			
305	310	315	320
Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser			
325	330	335	

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

340

345

350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

355

360

365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

370

375

380

Gln Ala Gly Ser Leu Val

385

390

<210> 145

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84).. (2726)

<400> 145

igcgggaagc gatgtagtag ctgccaggct gtccccgcc ctgccggcc cgagccccgc 60

gggccgccgc cgccaccgcc gcc atg aag aag cag ttc aac cgc atg aag cag 113

Met Lys Lys Gln Phe Asn Arg Met Lys Gln

1

5

10

ctg gct aac cag acc glg ggc aga gct gag aaa aca gaa gtc ctt agt 161

Leu Ala Asn Gln Thr Val Gly Arg Ala Glu Lys Thr Glu Val Leu Ser

15

20

25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata 209

Glu Asp Leu Leu Gln Ile Glu Arg Arg Leu Asp Thr Val Arg Ser Ile

30

35

40

tgc cac cat tcc cat aag cgc ttg gtg gca tgt ttc cag ggc cag cat	257
Cys His His Ser His Lys Arg Leu Val Ala Cys Phe Gln Gly Gln His	
45 50 55	
ggc acc gat gcc gag agg aga cac aaa aaa ctg cct ctg aca gct ctt	305
Gly Thr Asp Ala Glu Arg Arg His Lys Lys Leu Pro Leu Thr Ala Leu	
60 65 70	
gct caa aat atg caa gaa gca tcg act cag ctg gaa gac tct ctc ctg	353
Ala Gln Asn Met Gln Glu Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu	
75 80 85 90	
ggg aag atg ctg gag acg tgt gga gat gct gag aat cag ctg gct ctc	401
Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu	
95 100 105	
gag ctc tcc cag cac gaa gtc ttt gtt gag aag gag atc gtg gac cct	449
Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro	
110 115 120	
ctg tac ggc ata gct gag gtg gag att ccc aac atc cag aag cag agg	497
Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg	
125 130 135	
aag cag ctt gca aga ttg gtg tta gac tgg gat tca gtc aga gcc agg	545
Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg	
140 145 150	
tgg aac caa gct cac aaa tcc tca gga acc aac ttt cag ggg ctt cca	593
Trp Asn Gln Ala His Lys Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro	
155 160 165 170	
tca aaa ata gat act cta aag gaa gag atg gat gaa gct gga aat aaa	641
Ser Lys Ile Asp Thr Leu Lys Glu Glu Met Asp Glu Ala Gly Asn Lys	
175 180 185	

gta gaa cag tgc aag gat caa ctt gca gca gac atg tac aac ttt atg	689
Val Glu Gln Cys Lys Asp Gln Leu Ala Ala Asp Met Tyr Asn Phe Met	
190 195 200	
gcc aaa gaa ggg gag tat ggc aaa ttc ttt gtt acg tta tta gaa gcc	737
Ala Lys Glu Gly Glu Tyr Gly Lys Phe Phe Val Thr Leu Leu Glu Ala	
205 210 215	
caa gca gat tac cat aga aaa gca tta gca gtc tta gaa aag acc ctc	785
Gln Ala Asp Tyr His Arg Lys Ala Leu Ala Val Leu Glu Lys Thr Leu	
220 225 230	
ccc gaa atg cga gcc cat caa gat aag tgg gcg gaa aaa cca gcc ttt	833
Pro Glu Met Arg Ala His Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe	
235 240 245 250	
ggg act ccc cta gaa gaa cac ctg aag agg agc ggg cgc gag att gcg	881
Gly Thr Pro Leu Glu Glu His Leu Lys Arg Ser Gly Arg Glu Ile Ala	
255 260 265	
ctg ccc att gaa gcc tgt gtc atg ctg ctt ctg gag aca ggc atg aag	929
Leu Pro Ile Glu Ala Cys Val Met Leu Leu Leu Glu Thr Gly Met Lys	
270 275 280	
gag gag ggc ctt ttc cga att ggg gct ggg gcc tcc aag tta aag aag	977
Glu Glu Gly Leu Phe Arg Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys	
285 290 295	
ctg aaa gct gct ttg gac tgt ict act tct cac ctg gat gag ttc tat	1025
Leu Lys Ala Ala Leu Asp Cys Ser Thr Ser His Leu Asp Glu Phe Tyr	
300 305 310	
tca gac ccc cat gct gta gca ggt gct tta aaa tcc tat tta cgg gaa	1073
Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu	



315	320	325	330	
ttg cct gaa cct ttg atg act ttt aat ctg tat gaa gaa tgg aca caa	1121			
Leu Pro Glu Pro Leu Met Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln				
335	340	345		
gtt gca agt gig cag gat caa gac aaa aaa ctt caa gac ttg tgg aga	1169			
Val Ala Ser Val Gln Asp Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg				
350	355	360		
aca tgt cag aag ttg cca cca caa aat ttt gtt aac ttt aga tat ttg	1217			
Thr Cys Gln Lys Leu Pro Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu				
365	370	375		
atc aag ttc ctt gca aag ctt gct cag acc agc gat gtg aat aaa atg	1265			
Ile Lys Phe Leu Ala Lys Leu Ala Gln Thr Ser Asp Val Asn Lys Met				
380	385	390		
act ccc agc aac att gcg att gig tta ggc cct aac ttg tta tgg gcc	1313			
Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Ala				
395	400	405	410	
aga aat gaa gga aca ctt gct gaa atg gca gca gcc aca tcc gtc cat	1361			
Arg Asn Glu Gly Thr Leu Ala Glu Met Ala Ala Ala Thr Ser Val His				
415	420	425		
gtg gtt gca gig att gaa ccc atc att cag cat gcc gac tgg ttc ttc	1409			
Val Val Ala Val Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe				
430	435	440		
cct gaa gag gig gaa ttt aat gta tca gaa gca ttt gta cct ctc acc	1457			
Pro Glu Glu Val Glu Phe Asn Val Ser Glu Ala Phe Val Pro Leu Thr				
445	450	455		
acc ccg agt tct aat cac tca ttc cac act gga aac gac tct gac tcg	1505			
Thr Pro Ser Ser Asn His Ser Phe His Thr Gly Asn Asp Ser Asp Ser				

460	465	470	
ggg acc ctg gag agg aag cgg cct gct agc atg gcg gtg atg gaa gga	1553		
Gly Thr Leu Glu Arg Lys Arg Pro Ala Ser Met Ala Val Met Glu Gly			
475	480	485	490
gac ttg gtg aag aag gaa agc ttt ggt gtg aag ctt atg gac ttc cag	1601		
Asp Leu Val Lys Lys Glu Ser Phe Gly Val Lys Leu Met Asp Phe Gln			
495	500	505	
gcc cac cgg cgg ggt ggc act cta aat aga aag cac ata tcc ccc gct	1649		
Ala His Arg Arg Gly Gly Thr Leu Asn Arg Lys His Ile Ser Pro Ala			
510	515	520	
ttc cag ccg cca ctt ccg ccc aca gat ggc agc acc gtg gtg ccc gct	1697		
Phe Gln Pro Pro Leu Pro Pro Thr Asp Gly Ser Thr Val Val Pro Ala			
525	530	535	
ggc cca gag ccc cct ccc cag agc tct agg gct gaa agc agc tct ggg	1745		
Gly Pro Glu Pro Pro Pro Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly			
540	545	550	
ggt ggg act gtc ccc tct tcc gcg ggc ata ctg gag cag ggg ccg agc	1793		
Gly Gly Thr Val Pro Ser Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser			
555	560	565	570
cca ggc gac ggc agt cct ccc aaa ccg aag gac cct gta tct gca gct	1841		
Pro Gly Asp Gly Ser Pro Pro Lys Pro Lys Asp Pro Val Ser Ala Ala			
575	580	585	
gtg cca gca cca ggg aga aac aac agt cag ata gca tct ggc caa aat	1889		
Val Pro Ala Pro Gly Arg Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn			
590	595	600	
cag ccc cag gca gct gct ggc tcc cac cag ctc tcc atg ggc caa cct	1937		

Gln Pro Gln Ala Ala Ala Gly Ser His Gln Leu Ser Met Gly Gln Pro	
605	610
615	
cac aat gct gca ggg ccc agc ccg cat aca ctg cgc cga gct gtt aaa	1985
His Asn Ala Ala Gly Pro Ser Pro His Thr Leu Arg Arg Ala Val Lys	
620	625
630	
aaa ccc gct cca gca ccc ccg aaa ccg ggc aac cca cct cct ggc cac	2033
Lys Pro Ala Pro Ala Pro Pro Lys Pro Gly Asn Pro Pro Pro Gly His	
635	640
645	650
ccc ggg ggc cag agt tct tca gga aca tct cag cat cca ccc agt ctg	2081
Pro Gly Gly Gln Ser Ser Ser Gly Thr Ser Gln His Pro Pro Ser Leu	
655	660
665	
tca cca aag cca ccc acc cga agc ccc tct cct ccc acc cag cac acg	2129
Ser Pro Lys Pro Pro Thr Arg Ser Pro Ser Pro Pro Thr Gln His Thr	
670	675
680	
ggc cag cct cca ggc cag ccc tcc gcc ccc tcc cag ctc tca gca ccc	2177
Gly Gln Pro Pro Gly Gln Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro	
685	690
695	
cgg agg tac tcc agc agc ttg tct cca atc caa gct ccc aat cac cca	2225
Arg Arg Tyr Ser Ser Ser Leu Ser Pro Ile Gln Ala Pro Asn His Pro	
700	705
710	
ccg ccg cag ccc cct acg cag gcc acg cca ctg atg cac acc aaa ccc	2273
Pro Pro Gln Pro Pro Thr Gln Ala Thr Pro Leu Met His Thr Lys Pro	
715	720
725	730
aat agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga	2321
Asn Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly	
735	740
745	
clt gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt	2369

Leu Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser  
 750 755 760  
 act ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc 2417  
 Thr Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr  
 765 770 775  
 ctg gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta 2465  
 Leu Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu  
 780 785 790  
 ccg aga ccg aga cca gta cca aag cca agg aac cgg ccc agc gtg ccc 2513  
 Pro Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro  
 795 800 805 810  
 cca ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc 2561  
 Pro Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu  
 815 820 825  
 acc aac aca gca cca aca gct tcc aag ata gta aca gac tcc aat tcc 2609  
 Thr Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser  
 830 835 840  
 agg gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac 2657  
 Arg Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp  
 845 850 855  
 tca gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat 2705  
 Ser Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn  
 860 865 870  
 gat acc gag agc act gcc ctg tgaagaaagc cctttcccag cccctccacca 2756  
 Asp Thr Glu Ser Thr Ala Leu  
 875 880

ctccacccct ggcgagtgga gcaggggcag gcgaacctct ttctttgcag accgaacagt 2816  
 gaaaagcttt cagtggagga caaaggaggg cctcactgtg cgggacctgg ctttctgcac 2876  
 ggccaagga gaacctggag gccaccacta aagctgaatg acctgtgtct tgaagaagtt 2936  
 ggctttcttt acatgggaag gaaatcatgc caaaaaaatc caaaacaaag aagtacctgg 2996  
 agtggagaga gtattcctgc tgaaacgcgc ataggaagct ttgtlccctg ctgttaatgc 3056  
 gggcagcacc tacagcaact tggaatgagt aagaagcagt gcgttaacta tctatttaac 3116  
 aaaatgcgct cattatgcaa gtcgcctact ctctgttacc tggacgttca ttcttatgta 3176  
 ttaggaggga ggctgcgctc cticagactt gctgcagaat cattttgtat catgtatggt 3236  
 ctgtgtctcc ccagtcacct cagaacctatg cccatggatg gtgactgtct gctctgtcac 3296  
 ctcatcaaac tggatgtgac ccatgccgcc tcgttggatt gtcggaatgt agacagaaat 3356  
 gtactgttct ttttttttt tttaaacaat gtaattgcta ctgataagg accgaacatt 3416  
 attctagttt catgttttaac ttgaattaaa tataattctgt ggtttataatg 3466

<210> 146

<211> 881

<212> PRT

<213> Homo sapiens

<400> 146

Met	Lys	Lys	Gln	Phe	Asn	Arg	Met	Lys	Gln	Leu	Ala	Asn	Gln	Thr	Val
1				5						10				15	
Gly	Arg	Ala	Glu	Lys	Thr	Glu	Val	Leu	Ser	Glu	Asp	Leu	Leu	Gln	Ile
				20						25				30	
Glu	Arg	Arg	Leu	Asp	Thr	Val	Arg	Ser	Ile	Cys	His	His	Ser	His	Lys
				35						40				45	
Arg	Leu	Val	Ala	Cys	Phe	Gln	Gly	Gln	His	Gly	Thr	Asp	Ala	Glu	Arg
				50						55				60	
Arg	His	Lys	Lys	Leu	Pro	Leu	Thr	Ala	Leu	Ala	Gln	Asn	Met	Gln	Glu

65	70	75	80
Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu Gly Lys Met Leu Glu Thr			
	85	90	95
Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu Glu Leu Ser Gln His Glu			
	100	105	110
Val Phe Val Glu Lys Glu Ile Val Asp Pro Leu Tyr Gly Ile Ala Glu			
	115	120	125
Val Glu Ile Pro Asn Ile Gln Lys Gln Arg Lys Gln Leu Ala Arg Leu			
	130	135	140
Val Leu Asp Trp Asp Ser Val Arg Ala Arg Trp Asn Gln Ala His Lys			
145	150	155	160
Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro Ser Lys Ile Asp Thr Leu			
	165	170	175
Lys Glu Glu Met Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp			
	180	185	190
Gln Leu Ala Ala Asp Met Tyr Asn Phe Met Ala Lys Glu Gly Glu Tyr			
	195	200	205
Gly Lys Phe Phe Val Thr Leu Leu Glu Ala Gln Ala Asp Tyr His Arg			
	210	215	220
Lys Ala Leu Ala Val Leu Glu Lys Thr Leu Pro Glu Met Arg Ala His			
225	230	235	240
Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe Gly Thr Pro Leu Glu Glu			
	245	250	255
His Leu Lys Arg Ser Gly Arg Glu Ile Ala Leu Pro Ile Glu Ala Cys			
	260	265	270
Val Met Leu Leu Leu Glu Thr Gly Met Lys Glu Glu Gly Leu Phe Arg			
	275	280	285

Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys Leu Lys Ala Ala Leu Asp			
290	295	300	
Cys Ser Thr Ser His Leu Asp Glu Phe Tyr Ser Asp Pro His Ala Val			
305	310	315	320
Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro Leu Met			
	325	330	335
Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln Val Ala Ser Val Gln Asp			
	340	345	350
Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg Thr Cys Gln Lys Leu Pro			
	355	360	365
Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu Ile Lys Phe Leu Ala Lys			
	370	375	380
Leu Ala Gln Thr Ser Asp Val Asn Lys Met Thr Pro Ser Asn Ile Ala			
385	390	395	400
Ile Val Leu Gly Pro Asn Leu Leu Trp Ala Arg Asn Glu Gly Thr Leu			
	405	410	415
Ala Glu Met Ala Ala Ala Thr Ser Val His Val Val Ala Val Ile Glu			
	420	425	430
Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Glu Glu Val Glu Phe			
	435	440	445
Asn Val Ser Glu Ala Phe Val Pro Leu Thr Thr Pro Ser Ser Asn His			
	450	455	460
Ser Phe His Thr Gly Asn Asp Ser Asp Ser Gly Thr Leu Glu Arg Lys			
465	470	475	480
Arg Pro Ala Ser Met Ala Val Met Glu Gly Asp Leu Val Lys Lys Glu			
	485	490	495

Ser Phe Gly Val Lys Leu Met Asp Phe Gln Ala His Arg Arg Gly Gly  
 500 505 510  
 Thr Leu Asn Arg Lys His Ile Ser Pro Ala Phe Gln Pro Pro Leu Pro  
 515 520 525  
 Pro Thr Asp Gly Ser Thr Val Val Pro Ala Gly Pro Glu Pro Pro Pro  
 530 535 540  
 Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly Gly Gly Thr Val Pro Ser  
 545 550 555 560  
 Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser Pro Gly Asp Gly Ser Pro  
 565 570 575  
 Pro Lys Pro Lys Asp Pro Val Ser Ala Ala Val Pro Ala Pro Gly Arg  
 580 585 590  
 Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn Gln Pro Gln Ala Ala Ala  
 595 600 605  
 Gly Ser His Gln Leu Ser Met Gly Gln Pro His Asn Ala Ala Gly Pro  
 610 615 620  
 Ser Pro His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro  
 625 630 635 640  
 Pro Lys Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser  
 645 650 655  
 Ser Gly Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr  
 660 665 670  
 Arg Ser Pro Ser Pro Pro Thr Gln His Thr Gly Gln Pro Pro Gly Gln  
 675 680 685  
 Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro Arg Arg Tyr Ser Ser Ser  
 690 695 700  
 Leu Ser Pro Ile Gln Ala Pro Asn His Pro Pro Pro Gln Pro Pro Thr



705	710	715	720
Gln Ala Thr Pro Leu Met His Thr Lys Pro Asn Ser Gln Gly Pro Pro			
	725	730	735
Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu Glu Gln Pro Ser His			
	740	745	750
Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr Pro Pro Leu Gly Lys			
	755	760	765
Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu Ala Gly Gly Asn Pro			
	770	775	780
Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro Arg Pro Arg Pro Val			
785	790	795	800
Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro Pro Pro Gln Pro Pro			
	805	810	815
Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr Asn Thr Ala Pro Thr			
	820	825	830
Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg Val Ser Glu Pro His			
	835	840	845
Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser Ala Ser Lys Asp Val			
	850	855	860
Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp Thr Glu Ser Thr Ala			
865	870	875	880
Leu			

<210> 147

<211> 3021

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (140).. (1105)

<400> 147

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acagccctgtt ccaagigtgg cttaatccgt ctccaccacc agatctttct ccgtggattc 120  
ctctgctaag accgcigcc atg cca gtc acg gta acc cgc acc acc atc aca 172

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr

1

5

10

acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg atc gtc ggg 220  
Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly

15

20

25

tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag 268  
Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln

30

35

40

ctg gtc tct acc tgc gtc gcc ttc tcg ctg gtc gct agc gtc ggc gcc 316  
Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala

45

50

55

tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc 364  
Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys

60

65

70

75

ttc tcc gtc acc ctg atc atc ctc atc gtc gag ctg tgc ggg ctc cag 412  
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln

80

85

90

gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc 460  
Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys

95	100	105	
tat gcg ggc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc			508
Tyr Ala Gly Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr			
110	115	120	
tat gtc cag ttc ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc			556
Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala			
125	130	135	
gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg			604
Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val			
140	145	150	155
gcc tgg acc cgg gcc cgg ccc ggc gag atc act ggc tat atg gcc acc			652
Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr			
160	165	170	
gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc			700
Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile			
175	180	185	
ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg gcc ctg			748
Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu			
190	195	200	
gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc			796
Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile			
205	210	215	
gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc			844
Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro			
220	225	230	235
ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat			892
Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr			

240	245	250	
gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat	940		
Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr			
255	260	265	
ggc ggc cag cct cgg cgc tgc aga gat gta agc tgc agc cgc agc cat	988		
Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His			
270	275	280	
gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg	1036		
Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu			
285	290	295	
acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc	1084		
Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala			
300	305	310	315
cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct cccgttcct	1135		
His Leu Val Phe Val Lys Val			
320			
ctccaaccctc ttgtttcttc ttgcccagagt tttctttatg gactacttct ttccctccgcc	1195		
tttccctctgt ttccctcttc ctgtctcccc tccctccac cttttcttt ccttcccaat	1255		
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ccttccctgtg ttgttttgtt gccacatcc tgttttcacc cctgagctgt ttctcttttt	1375		
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cgcagtggtg cgatctcgac tcactgcaac ccccgccctc tgggttcaag cgattctct	1495		
gccccagcct cccaagtagc tgggaggaca ggtgtgagct gccgcacca gcctgtttct	1555		
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gcctgttttg caagcacctt ctccgtgtgc ctggggagcc ctgagacttc ttctctctct	1675		
tgccctccacc caccctcaaa ggtgtgagc tcacatccac accccttgca gccgtccatg	1735		

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acataatata atataatatt ggaggicagt aatttccaat gggcgggagg cattaagcac 1975  
cgacctggg tccctaggcc ccgctggca ctacgccttg ccagagattg gctccagaat 2035  
ttttgccagg cttacagaac acccactgcc tagaggccat cttaaaggaa gcaggggctg 2095  
gatgccttcc atcccaacta ttctctgtgg taigaaaaag aaaaaaaaaa aaaaagaagg 2155  
agtcggggcc gggcgtgggt gtcacgcct gtaatcccag cactttggga gaccaagtca 2215  
ggcaatcatt tgaagtcagg agttcaagac cagcctggcc aacatggiga aagcatgtct 2275  
ctattaaaaa taaaaaatt agccgggcgt ggtggcgggc gcctgtaatc ccaggtatit 2335  
ggggggactg agacaggaga atcccttcaa cccgggaggt ggaggttgca gtaagtcaag 2395  
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gaatcgagc agaaccaca ggaatlgaa gacaactgtc tgaagtatit gtgagggaca 2515  
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atgtataaat atataatit tttttttta aatccttgga gcttctgggt cctatcagtt 2935  
ccgttgttta atcgtagaac cgttgtccct tccccattc ccgtatccat catgttcttt 2995  
ttctttttaa tatcaatata aaaggt 3021

<210> 148

<211> 322

<212> PRT

<213> Homo sapiens

<400> 148

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Ser	
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Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg	Ala	Leu
				20				25					30		
Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	Ser	Thr	Cys
				35				40					45		
Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	Thr	Gly	Ser	Met
				50				55					60		
Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	Phe	Ser	Val	Thr	Leu
				65				70					75		80
Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	Gln	Ala	Arg	Phe	Pro	Leu
				85				90					95		
Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	Ala	Cys	Tyr	Ala	Gly	Leu	Phe
				100				105					110		
Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu
				115				120					125		
Ser	His	Gly	Arg	Ser	Arg	Asp	His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser
				130				135					140		
Cys	Ile	Ala	Cys	Val	Ala	Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala
				145				150					155		160
Arg	Pro	Gly	Glu	Ile	Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu
				165				170					175		
Lys	Val	Leu	Glu	Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser
				180				185					190		
Asp	Pro	Asn	Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala
				195				200					205		

Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn  
 210 215 220  
 Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
 225 230 235 240  
 Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val  
 245 250 255  
 Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg  
 260 265 270  
 Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys  
 275 280 285  
 Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu  
 290 295 300  
 Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val  
 305 310 315 320  
 Lys Val

<210> 149

<211> 4409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (39).. (2027)

<400> 149

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Met Ser Trp Leu Ser Ser

1

5

tcc cag gga gtg gta cta aca gcc tac cac ccc agc ggc aag gac cag	104
Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln	
10 15 20	
gcc gtc ggg aac agc cat gca aag gca ggg gag gaa gcc acc tcg agt	152
Ala Val Gly Asn Ser His Ala Lys Ala Gly Glu Glu Ala Thr Ser Ser	
25 30 35	
cgc aga tat ggc cag tac act atg aac cag gaa agc acc acc atc aaa	200
Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln Glu Ser Thr Thr Ile Lys	
40 45 50	
gtt atg gag aag cct cca ttt gat cga tca att tcc cag gat tct ttg	248
Val Met Glu Lys Pro Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu	
55 60 65 70	
gat gaa cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc aag	296
Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys	
75 80 85	
aaa tct agt gaa aac agc caa gaa gat caa gag gtg gtt gtt gtc aaa	344
Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys	
90 95 100	
gag cct gat gag gga gaa ttg gaa gaa gag tgg ctt aaa gag gcc ggt	392
Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu Trp Leu Lys Glu Ala Gly	
105 110 115	
tta tcc aat ctc ttc gga gag tct gct gga gat cca cag gaa agc att	440
Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile	
120 125 130	
gtg ttt tta tca aca ttg acg cgg acc cag gca gca gca gtt cag aag	488
Val Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys	



135	140	145	150	
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac aaa cag tac				536
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln Tyr				
	155	160	165	
cag att cct gac gtc aga gac ata ttt gct caa cag aga gaa tca aaa				584
Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu Ser Lys				
	170	175	180	
gaa aca gct cca ggt ggc act gaa tcg cag tca ctt aga aca aat gaa				632
Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg Thr Asn Glu				
	185	190	195	
aac aaa tac caa gga aga gat gac gag gca tct aac ctt gtt ggt gaa				680
Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu				
	200	205	210	
gag aag ctg atc cca cct gag gag acg cct gcc cct gaa aca gac atc				728
Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr Asp Ile				
	215	220	225	230
aac ctg gag gta tca ttt gcc gag caa gca ctc aat cag aaa gag agc				776
Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu Asn Gln Lys Glu Ser				
	235	240	245	
tcc aag gag aaa atc cag aag agc aaa ggc gat gat gcc aca tta cct				824
Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly Asp Asp Ala Thr Leu Pro				
	250	255	260	
agt ttc aga ttg cca aaa gac aaa acg ggt acc aca agg att ggt gac				872
Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp				
	265	270	275	
ctc gca ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att gag				920
Leu Ala Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile Glu				

280	285	290	
ctg act gcc ctc tat gat gta ttg ggt att gag ctg aaa caa caa aaa			968
Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu Lys Gln Gln Lys			
295	300	305	310
gct gtg aaa atc aaa aca aaa gat tct ggt ctt ttt tgc gtt cca ttg			1016
Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu			
315	320	325	
aca gcg cta tta gaa caa gat cag agg aaa gta cca gga atg cga ata			1064
Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile			
330	335	340	
ccc ttg atc ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg			1112
Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu			
345	350	355	
gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att aga atc aag			1160
Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys			
360	365	370	
aat ctt tgc caa gaa cta gaa gca aag ttt tat gaa ggg act ttt aat			1208
Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn			
375	380	385	390
tgg gaa agt gtc aaa cag cat gat gcc gcc agc ctg ctg aag ctc ttc			1256
Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu Phe			
395	400	405	
att cgg gag ttg ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc			1304
Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala			
410	415	420	
ttt cag gct gtc cag aat ctt cca acc aag aag cag caa cta cag gct			1352

Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu Gln Ala	
425	430
435	
ttg aac ctt ctt ggc atc ctc cta cct gat gca aac agg gac aca ctg	1400
Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp Ala Asn Arg Asp Thr Leu	
440	445
450	
aag gcc ctt ctt gaa ttt ctc caa aga gta ata gat aat aaa gaa aaa	1448
Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile Asp Asn Lys Glu Lys	
455	460
465	470
aat aaa atg aca gtc atg aat gta gca atg gtc atg gcc ccg aat ctc	1496
Asn Lys Met Thr Val Met Asn Val Ala Met Val Met Ala Pro Asn Leu	
475	480
485	
ttt atg tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa ttt	1544
Phe Met Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu Phe	
490	495
500	
gta atg gca gct ggg aca gca aat acc atg cac tta ttg att aag tac	1592
Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu Leu Ile Lys Tyr	
505	510
515	
caa aaa ctt ctg tgg aca att ccc aag ttt att gta aac caa gtg agg	1640
Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe Ile Val Asn Gln Val Arg	
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aag caa aac acg gaa aat cat aaa aag gat aaa aga gcc atg aag aaa	1688
Lys Gln Asn Thr Glu Asn His Lys Lys Asp Lys Arg Ala Met Lys Lys	
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ttg ctg aag aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat	1736
Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp	
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Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln  
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 Ala Pro His Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu  
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 Leu Lys Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly  
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 Val Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly  
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 Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys Asp  
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<211> 663

<212> PRT

<213> Homo sapiens

<400> 150

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Glu	Glu	Ala	Thr	Ser	Ser	Arg	Arg	Tyr	Gly	Gln	Tyr	Thr	Met	Asn	Gln
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Glu	Ser	Thr	Thr	Ile	Lys	Val	Met	Glu	Lys	Pro	Pro	Phe	Asp	Arg	Ser
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Ile	Ser	Gln	Asp	Ser	Leu	Asp	Glu	Leu	Ser	Met	Glu	Asp	Tyr	Trp	Ile
				65					70					75	
Glu	Leu	Glu	Asn	Ile	Lys	Lys	Ser	Ser	Glu	Asn	Ser	Gln	Glu	Asp	Gln
				85					90					95	
Glu	Val	Val	Val	Val	Lys	Glu	Pro	Asp	Glu	Gly	Glu	Leu	Glu	Glu	Glu
				100					105					110	
Trp	Leu	Lys	Glu	Ala	Gly	Leu	Ser	Asn	Leu	Phe	Gly	Glu	Ser	Ala	Gly
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Asp	Pro	Gln	Glu	Ser	Ile	Val	Phe	Leu	Ser	Thr	Leu	Thr	Arg	Thr	Gln
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Ala	Ala	Ala	Val	Gln	Lys	Arg	Val	Glu	Thr	Val	Ser	Gln	Thr	Leu	Arg
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Lys	Lys	Asn	Lys	Gln	Tyr	Gln	Ile	Pro	Asp	Val	Arg	Asp	Ile	Phe	Ala
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Gln	Gln	Arg	Glu	Ser	Lys	Glu	Thr	Ala	Pro	Gly	Gly	Thr	Glu	Ser	Gln
			180					185					190		
Ser	Leu	Arg	Thr	Asn	Glu	Asn	Lys	Tyr	Gln	Gly	Arg	Asp	Asp	Glu	Ala
		195					200					205			
Ser	Asn	Leu	Val	Gly	Glu	Glu	Lys	Leu	Ile	Pro	Pro	Glu	Glu	Thr	Pro
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Ala	Pro	Glu	Thr	Asp	Ile	Asn	Leu	Glu	Val	Ser	Phe	Ala	Glu	Gln	Ala
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Leu	Asn	Gln	Lys	Glu	Ser	Ser	Lys	Glu	Lys	Ile	Gln	Lys	Ser	Lys	Gly
				245						250				255	
Asp	Asp	Ala	Thr	Leu	Pro	Ser	Phe	Arg	Leu	Pro	Lys	Asp	Lys	Thr	Gly
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Thr	Thr	Arg	Ile	Gly	Asp	Leu	Ala	Pro	Gln	Asp	Met	Lys	Lys	Val	Cys
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His	Leu	Ala	Leu	Ile	Glu	Leu	Thr	Ala	Leu	Tyr	Asp	Val	Leu	Gly	Ile
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Leu	Phe	Cys	Val	Pro	Leu	Thr	Ala	Leu	Leu	Glu	Gln	Asp	Gln	Arg	Lys
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Val	Pro	Gly	Met	Arg	Ile	Pro	Leu	Ile	Phe	Gln	Lys	Leu	Ile	Ser	Arg
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Ile	Glu	Glu	Arg	Gly	Leu	Glu	Thr	Glu	Gly	Leu	Leu	Arg	Ile	Pro	Gly
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Ala	Ala	Ile	Arg	Ile	Lys	Asn	Leu	Cys	Gln	Glu	Leu	Glu	Ala	Lys	Phe
			370				375						380		
Tyr	Glu	Gly	Thr	Phe	Asn	Trp	Glu	Ser	Val	Lys	Gln	His	Asp	Ala	Ala
385						390					395			400	
Ser	Leu	Leu	Lys	Leu	Phe	Ile	Arg	Glu	Leu	Pro	Gln	Pro	Leu	Leu	Ser
						405				410				415	
Val	Glu	Tyr	Leu	Lys	Ala	Phe	Gln	Ala	Val	Gln	Asn	Leu	Pro	Thr	Lys
			420					425						430	
Lys	Gln	Gln	Leu	Gln	Ala	Leu	Asn	Leu	Leu	Gly	Ile	Leu	Leu	Pro	Asp
			435					440						445	
Ala	Asn	Arg	Asp	Thr	Leu	Lys	Ala	Leu	Leu	Glu	Phe	Leu	Gln	Arg	Val
			450				455							460	
Ile	Asp	Asn	Lys	Glu	Lys	Asn	Lys	Met	Thr	Val	Met	Asn	Val	Ala	Met
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Val	Met	Ala	Pro	Asn	Leu	Phe	Met	Cys	His	Ala	Leu	Gly	Leu	Lys	Ser
						485				490				495	
Ser	Glu	Gln	Arg	Glu	Phe	Val	Met	Ala	Ala	Gly	Thr	Ala	Asn	Thr	Met
			500					505						510	
His	Leu	Leu	Ile	Lys	Tyr	Gln	Lys	Leu	Leu	Trp	Thr	Ile	Pro	Lys	Phe
			515					520						525	
Ile	Val	Asn	Gln	Val	Arg	Lys	Gln	Asn	Thr	Glu	Asn	His	Lys	Lys	Asp
			530					535						540	
Lys	Arg	Ala	Met	Lys	Lys	Leu	Leu	Lys	Lys	Met	Ala	Tyr	Asp	Arg	Glu



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 Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp Val Pro Gln  
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 Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala  
                     580                      585                      590  
 Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu Ala Arg Phe  
                     595                      600                      605  
 Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys Gly Glu Val  
                     610                      615                      620  
 Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp  
 625                      630                      635                      640  
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<220>

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Pro Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp	
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Asp Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn	
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Gly Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro	
65 70 75	
agc ctg gat gag ctg aat ccc aaa agt act gtg gat ttg ctc ctt ttt	287
Ser Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe	
80 85 90 95	
gac gca ggt aca tcc tcc ttc acc gaa tcc agc tca gcc acc acg aat	335
Asp Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn	
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agc act ggc aac atc ttc gat gag ctt cca gtc aca aac ggg ctc cac	383
Ser Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His	
115 120 125	
gca gag ccg ccg gtc agg cgg gac aac ccc ttc ttc aga agc aag cgc	431
Ala Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg	
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tcc tac agt ctc tcg gaa ctc tcc gtc ctc caa gcc aag tcc gac gct	479
Ser Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala	

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Pro Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu			
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caa ttt cag agc cgg gag gat ttt cga act gcc tgg cta aac cac agg	575		
Gln Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg			
180	185	190	
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Lys Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro			
195	200	205	
ggt tgg ggc cag acc caa gcc gtg gag aca aac atc gtg tgc aag ctg	671		
Gly Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu			
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Asp Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile			
225	230	235	
cac gtg ccc gag ggc cac gtc gcc cct ggg gag acc cag cag atc tcc	767		
His Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser			
240	245	250	255
atg aaa gcc ctg ctg gac ccc ccg ctg gag ctc aac agt gac agg tcc	815		
Met Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser			
260	265	270	
tgc agc atc agc cct gtg ctg gag gtc aag ctg agc aac ctg gag gtg	863		
Cys Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val			
275	280	285	
aaa acc tct atc atc ttg gag atg aaa gtg tca gcc gag ata aaa aat	911		
Lys Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn			

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Asp Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp			
305	310	315	
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Ser Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly			
320	325	330	335
gac acg gtc cag gca cag ctg cac aac ctg gag ccc tgt atg tac gtg			1055
Asp Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val			
	340	345	350
gct gtc gtg gcc cat ggc cca agc atc ctc tac cct tcc acc gtg tgg			1103
Ala Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp			
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Asp Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His			
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Ile His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys			
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Ala Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn			
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cct gcc ccg gtg gcc ctg cag ctg tgg ggg aag cac cag ttc gtt ttg			1295
Pro Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu			
	420	425	430
tcc agg ccc cag gat ctc aag gtc tgt atg ttt tcc aat atg acg aat			1343



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agg ctc cgg ggc cag ctg tgg acc aag gag tgg tac atc ggc tac tac	1823
Arg Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr	
595	600
cag ggc agg gtg ggc ctc gtg cac acc aag aac gtg ctg gtg gtc ggc	1871
Gln Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly	
610	615
agg gcc cgg ccc agc ctg tgc tgc ggc ccc gag ctg agc acc tgc gtg	1919
Arg Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val	
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ctg ctg gag cag atc ctg cgg ccc tgc aaa ttc ctc acg tac atc tat	1967
Leu Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr	
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Ala Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser	
660	665
ttc gct gac gcc ctg ggc tac gtg aac ctg ccg ctc acc ttt ttc tgc	2063
Phe Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys	
675	680
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Arg Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu	
690	695
aag ctg aag gag gac tgt aac aac act gag aac aaa gaa cgg aag tcc	2159
Lys Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser	
705	710
	715

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Glu Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val	
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Ser Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn	
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Gly Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu	
785                      790                      795	
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Glu Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg	
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Trp Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val	
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Leu Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile	
850                      855                      860	

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gaacaaacat tagctatitit atgctgcaag aaccaggaca cacaattcgc caatcatccc 4211  
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 tatcacctit tccccaaaga agaaacaaaa ccagttgcac cttaaaccat ggataatitit 4331  
 tcctcagggg cttaaataag tttcctatgc aacgtgtctt gtagcacaaa taaaattcta 4391  
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<210> 152

<211> 863

<212> PRT

<213> Homo sapiens

<400> 152

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Ser	Thr	Leu	Ser	Asp	Ser	Gly	Met	Ile	Asp	Asn	Leu	Pro	Asp	Ser	Pro
				20					25					30	
Asp	Glu	Val	Ala	Lys	Glu	Leu	Glu	Leu	Leu	Gly	Gly	Trp	Thr	Asp	Asp
				35					40					45	
Lys	Lys	Val	Pro	Gly	Arg	Met	Tyr	Ser	Asn	Asn	Pro	Phe	Trp	Asn	Gly
				50					55					60	
Val	Gln	Thr	Asn	Pro	Phe	Leu	Asn	Gly	Asn	Val	Pro	Val	Met	Pro	Ser
				65					70					75	
Leu	Asp	Glu	Leu	Asn	Pro	Lys	Ser	Thr	Val	Asp	Leu	Leu	Leu	Phe	Asp
				85					90					95	
Ala	Gly	Thr	Ser	Ser	Phe	Thr	Glu	Ser	Ser	Ser	Ala	Thr	Thr	Asn	Ser
				100					105					110	
Thr	Gly	Asn	Ile	Phe	Asp	Glu	Leu	Pro	Val	Thr	Asn	Gly	Leu	His	Ala

115	120	125	
Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg Ser			
130	135	140	
Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala Pro			
145	150	155	160
Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu Gln			
	165	170	175
Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg Lys			
	180	185	190
Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro Gly			
	195	200	205
Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu Asp			
	210	215	220
Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile His			
225	230	235	240
Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser Met			
	245	250	255
Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser Cys			
	260	265	270
Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val Lys			
	275	280	285
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp			
	290	295	300
Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser			
305	310	315	320
Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp			
	325	330	335

Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala			
340	345	350	
Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp			
355	360	365	
Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His Ile			
370	375	380	
His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala			
385	390	395	400
Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro			
405	410	415	
Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser			
420	425	430	
Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr			
435	440	445	
Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu			
450	455	460	
Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn			
465	470	475	480
Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp			
485	490	495	
Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro			
500	505	510	
Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys			
515	520	525	
Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys			
530	535	540	

Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys  
545 550 555 560  
Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu  
565 570 575  
Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg  
580 585 590  
Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr Gln  
595 600 605  
Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg  
610 615 620  
Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val Leu  
625 630 635 640  
Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala  
645 650 655  
Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe  
660 665 670  
Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg  
675 680 685  
Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys  
690 695 700  
Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe  
705 710 715 720  
Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu  
725 730 735  
Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu  
740 745 750  
Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val Ser

755	760	765
Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn Gly		
770	775	780
Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu Leu		
785	790	795
Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu		
805	810	815
Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp		
820	825	830
Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu		
835	840	845
Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile		
850	855	860

<210> 153

<211> 2194

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133).. (1125)

<400> 153

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 gcgggcgccc gc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc cct 171

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro

1

5

10

ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg gtc	219
Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val	
15 20 25	
aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc ttc	267
Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe	
30 35 40 45	
agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag ccc	315
Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro	
50 55 60	
cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac gcg	363
Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala	
65 70 75	
ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga gca	411
Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala	
80 85 90	
aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct gtc	459
Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val	
95 100 105	
tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg cga	507
Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg	
110 115 120 125	
ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca gca	555
Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala	
130 135 140	
aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc cta	603
Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu	

145	150	155	
agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc ttt			651
Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe			
160	165	170	
gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa atg			699
Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met			
175	180	185	
tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct ttc			747
Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe			
190	195	200	205
ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata			795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile			
210	215	220	
aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg			843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly			
225	230	235	
aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg			891
Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met			
240	245	250	
gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg tgt			939
Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys			
255	260	265	
gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc tac			987
Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr			
270	275	280	285
ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act gtt			1035
Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val			

290	295	300	
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Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser			
305	310	315	
tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc			1125
Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe			
320	325	330	
tagactttca cggtagggacg aaacgggttc agaaactgcc aggggcctca tacagggata			1185
tcaaaataacc ctttgtgcta gcccaggccc tggggaatca ggtgactcac acaaatgcaa			1245
tagttggica ctgcattttt acctgaacca aagctaaacc cggtgttgcc accatgcacc			1305
atggcatgcc agagtccaac actgttgcic ttgaaaatct gggcttgaaa aaacgcacaa			1365
gagccccctgc cctgccctag ctgaggcaca caggagacc cagtaggat aagcacagat			1425
tgaattgtac agtttgcaga tgcagatgia aatgcatggg acatgcatga taactcagag			1485
ttgacatttt aaaacttgcc acacttattt caaatatttg tactcagcta tgttaacaatg			1545
tactgtagac atcaaacttg tggccatact aataaaatta ttaaaaggag cactaaagga			1605
aaactgtgtg ccaagcatca tatcctaagg catacggaat ttggggaagc caccatgcaa			1665
tccagigagg cticagtga cagcaaccaa aatggtaggg aggtcttgaa gccaatgagg			1725
gatttatagc atcttgaata gagagctgca aaccaccagg gggcagagt gcatttttcc			1785
aggcttttta ggaagctctg caacagatgt gatctgatca taggcaatta gaactggaag			1845
aaacttccaa aaatacttag gttgtccic attttacaaa tgaggaaact aaactctgtg			1905
gaagggaagg ggttgcctca aaagtcacag cttagctggg cacagtggct catgccgata			1965
atcccagcaa ttcagaaagc tgaggcagga ggattacttg aggccagact gggcaataia			2025
gcaagacccc atctctaaaa aattaggcat ggtagtgcat gcctgtattc ccagctactic			2085
aggaggtiga ggtgggagga tcactlgagc ccagaagttc aaggctgcaa tgagccatga			2145
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<210> 154



<211> 331

<212> PRT

<213> Homo sapiens

<400> 154

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20 25 30  
Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu  
35 40 45  
Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg  
50 55 60  
Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn  
65 70 75 80  
Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val  
85 90 95  
Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His  
100 105 110  
Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp  
115 120 125  
Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg  
130 135 140  
Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala  
145 150 155 160  
Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys  
165 170 175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu			
180	185	190	
Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu			
195	200	205	
Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu			
210	215	220	
Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg			
225	230	235	240
Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu			
245	250	255	
Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser			
260	265	270	
Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys			
275	280	285	
Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe			
290	295	300	
Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr			
305	310	315	320
Asp Ser Met Val Glu Asp Cys Glu Pro His Phe			
325	330		

<210> 155

<211> 3377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44).. (1666)

<400> 155

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cag cga gtg gga gca gct gcc tca aga gga gca gat gat gcc atg gag 103
Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp Asp Ala Met Glu
    5             10             15             20
agc agc aag cct ggt cca gtg cag gtt gtt ttg gtt cag aaa gat caa 151
Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val Gln Lys Asp Gln
             25             30             35
cat tcc ttt gag cta gat gag aaa gcc ttg gcc agc atc ctc ttg cag 199
His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser Ile Leu Leu Gln
             40             45             50
gac cac atc cga gat ctt gat gtg gtg gtg gtt tca gtg gct ggt gcc 247
Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser Val Ala Gly Ala
             55             60             65
ttc cga aag ggc aag tcc ttc att ctg gat ttt atg cta cga tac tta 295
Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu
             70             75             80
tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa 343
Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu
             85             90             95             100
gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc 391
Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr
             105             110             115
act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt 439
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Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val Glu Lys Pro Gly	
120	125
130	
ggg aag aag gtt gca gtt gtt ctg atg gat acc cag ggg gca ttt gac	487
Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln Gly Ala Phe Asp	
135	140
145	
agc cag tca act gtg aaa gac tgt gct acc atc ttt gct cta agc act	535
Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr	
150	155
160	
atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa	583
Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu	
165	170
175	180
gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca	631
Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr Gly Arg Leu Ala	
185	190
195	
atg gat gaa att ttc caa aag cct ttc cag aca ctg atg ttt ttg gtt	679
Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu Met Phe Leu Val	
200	205
210	
aga gat tgg agt ttc cct tat gaa tat agc tat gga ctc caa gga gga	727
Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly Leu Gln Gly Gly	
215	220
225	
atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa	775
Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu His Gln His Glu	
230	235
240	
gaa att cag aat gtt cga aat cac att cac tca tgt ttc tcc gat gtc	823
Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys Phe Ser Asp Val	
245	250
255	260

acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct	871
Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro	
265 270 275	
gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag	919
Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln	
280 285 290	
tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa	967
Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser Lys Leu Met Glu	
295 300 305	
aag gag atc aat ggc tca aag gtc acc tgt cgg gga cta ctg gag tat	1015
Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly Leu Leu Glu Tyr	
310 315 320	
ttt aag gca tat att aaa att tat caa gga gaa gat ctg cct cac ccc	1063
Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp Leu Pro His Pro	
325 330 335 340	
aag tcc atg ctt cag gcc act gct gaa gcc aac aac tta gca gct gca	1111
Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Ala	
345 350 355	
gcc tct gcc aag gac att tat tat aac aac atg gaa gag gtt tgt ggg	1159
Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu Glu Val Cys Gly	
360 365 370	
gga gag aaa cct tat ttg tct cca gac att cta gag gag aag cac tgt	1207
Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu Glu Lys His Cys	
375 380 385	
gaa ttc aaa caa ctt gct ctg gac cat ttt aag aag acc aag aag atg	1255
Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys Thr Lys Lys Met	
390 395 400	

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 Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu Leu Glu Glu Glu  
 405 410 415 420  
 atc aag gaa tta tat gag aac ttc tgc aag cac aat ggt agc aag aac 1351  
 Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn Gly Ser Lys Asn  
 425 430 435  
 gtc ttc agc acc ttc cga acc cct gca gtg ctg ttc acg ggc att gta 1399  
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 Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu Leu Ile Ala Leu  
 470 475 480  
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 Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr Arg Glu Leu Gly  
 485 490 495 500  
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 Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu Gln Ala Ser Ser  
 505 510 515  
 cat atc ggt aat tcc act cag gcc act gtg agg gat gca gtt gtt gga 1639  
 His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp Ala Val Val Gly  
 520 525 530  
 aga cca tcc atg gat aaa aaa gct caa tagcatctta acgtgaagat 1686  
 Arg Pro Ser Met Asp Lys Lys Ala Gln

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 caagaattct ggctgtttac ctgagactca gaccctgaa atgttgccaa attcttcaaa 3066  
 taactgtttg ggggttgggg ggagatgaaa gagagtcgct tttgttttac agttaaagac 3126  
 atccaatatc ttaaaaagga gtttccctt agaaacacac acaccttcc tcttgcctaa 3186  
 aagatctcac tccatgatac tgtgtaaaa attttgcac tgttgtgaag ttttttgac 3246

ttttttcigt acataactgt gtctcagag cigaatgitt atatcttttg ctgtgcaaaa 3306  
 gaaacatgta aaatgttggt cagttgtata tacagaaatg tgtataaaac attttgttat 3366  
 tttttaaaag t 3377

<210> 156

<211> 541

<212> PRT

<213> Homo sapiens

<400> 156

Met	Leu	Ser	Pro	Gln	Arg	Val	Gly	Ala	Ala	Ala	Ser	Arg	Gly	Ala	Asp
1				5				10						15	
Asp	Ala	Met	Glu	Ser	Ser	Lys	Pro	Gly	Pro	Val	Gln	Val	Val	Leu	Val
			20					25						30	
Gln	Lys	Asp	Gln	His	Ser	Phe	Glu	Leu	Asp	Glu	Lys	Ala	Leu	Ala	Ser
		35					40						45		
Ile	Leu	Leu	Gln	Asp	His	Ile	Arg	Asp	Leu	Asp	Val	Val	Val	Val	Ser
	50					55					60				
Val	Ala	Gly	Ala	Phe	Arg	Lys	Gly	Lys	Ser	Phe	Ile	Leu	Asp	Phe	Met
65				70						75				80	
Leu	Arg	Tyr	Leu	Tyr	Ser	Gln	Lys	Glu	Ser	Gly	His	Ser	Asn	Trp	Leu
			85							90				95	
Gly	Asp	Pro	Glu	Glu	Pro	Leu	Thr	Gly	Phe	Ser	Trp	Arg	Gly	Gly	Ser
		100						105						110	
Asp	Pro	Glu	Thr	Thr	Gly	Ile	Gln	Ile	Trp	Ser	Glu	Val	Phe	Thr	Val
		115					120							125	
Glu	Lys	Pro	Gly	Gly	Lys	Lys	Val	Ala	Val	Val	Leu	Met	Asp	Thr	Gln
	130						135							140	



Gly	Ala	Phe	Asp	Ser	Gln	Ser	Thr	Val	Lys	Asp	Cys	Ala	Thr	Ile	Phe
145					150					155					160
Ala	Leu	Ser	Thr	Met	Thr	Ser	Ser	Val	Gln	Ile	Tyr	Asn	Leu	Ser	Gln
				165					170						175
Asn	Ile	Gln	Glu	Asp	Asp	Leu	Gln	Gln	Leu	Gln	Leu	Phe	Thr	Glu	Tyr
			180					185						190	
Gly	Arg	Leu	Ala	Met	Asp	Glu	Ile	Phe	Gln	Lys	Pro	Phe	Gln	Thr	Leu
		195						200					205		
Met	Phe	Leu	Val	Arg	Asp	Trp	Ser	Phe	Pro	Tyr	Glu	Tyr	Ser	Tyr	Gly
	210						215						220		
Leu	Gln	Gly	Gly	Met	Ala	Phe	Leu	Asp	Lys	Arg	Leu	Gln	Val	Lys	Glu
225					230					235					240
His	Gln	His	Glu	Glu	Ile	Gln	Asn	Val	Arg	Asn	His	Ile	His	Ser	Cys
			245						250					255	
Phe	Ser	Asp	Val	Thr	Cys	Phe	Leu	Leu	Pro	His	Pro	Gly	Leu	Gln	Val
		260							265					270	
Ala	Thr	Ser	Pro	Asp	Phe	Asp	Gly	Lys	Leu	Lys	Asp	Ile	Ala	Gly	Glu
		275						280						285	
Phe	Lys	Glu	Gln	Leu	Gln	Ala	Leu	Ile	Pro	Tyr	Val	Leu	Asn	Pro	Ser
	290						295							300	
Lys	Leu	Met	Glu	Lys	Glu	Ile	Asn	Gly	Ser	Lys	Val	Thr	Cys	Arg	Gly
305					310					315					320
Leu	Leu	Glu	Tyr	Phe	Lys	Ala	Tyr	Ile	Lys	Ile	Tyr	Gln	Gly	Glu	Asp
				325						330				335	
Leu	Pro	His	Pro	Lys	Ser	Met	Leu	Gln	Ala	Thr	Ala	Glu	Ala	Asn	Asn
		340							345					350	



<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45).. (563)

<400> 157

ggaacacggc acccgcactg cgcgtcatgg tgcaggcctg gtat atg gac gac gcc 56

Met Asp Asp Ala

1

ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg 104

Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val

5 10 15 20

ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat 152

Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp

25 30 35

gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag 200

Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu

40 45 50

agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta 248

Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu

55 60 65

cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac 296

Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His

70 75 80

ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat 344

Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp

85 90 95 100

gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga 392  
 Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly  
 105 110 115  
 gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac 440  
 Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp  
 120 125 130  
 gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa ccg gtg 488  
 Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val  
 135 140 145  
 tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag 536  
 Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln  
 150 155 160  
 tac gtg aaa ttt ctg gca cag acc gcc tagcagtgt gcttggaac 583  
 Tyr Val Lys Phe Leu Ala Gln Thr Ala  
 165 170  
 taacacgtgc ctgtaaaagg tccccaatgt aatgactgag cagaaaatca atcactttct 643  
 ctttgctttt agaggatagc cttagaggcta gattatcttt cctttgtaag attatttgat 703  
 cagaatatit tgtaatgaaa ggaatctagaa agcaacttgg aagtgtaaag agtcaccttc 763  
 attttctgta actcaatcaa gactgggtggg tccatggccc tgggttagtt catgcattca 823  
 gttgagtcct aaatgaaagt ttcattctcc gaaatgcagt tccatagatg cccatctgga 883  
 cgtgatgccg cgcctgccgt gtaagaaggt gcaatcctag ataacacagc tagccagata 943  
 gaagacacit ttttctccaa aatgatgcct tgggggtggg agtggtaggg ggaagagctc 1003  
 ccaccctaag gggcacacac tgagtgcct atgccacttc ctgttcaaa ataaagtaac 1063  
 tgccttaatc ttatactcat ggcttggagt taccittatat tcaggatata gtgatatit 1123  
 gccgtgtttg ttaaaattgc cccatttaga ttccttctat aattgttctt atagataagt 1183  
 aatttatata tgagctgtgt tagtatitit tcagtgtgag atctctggat tctttcacia 1243

taaagctgtt gaattttaac aggagiatia gtacataaat tttctactca acaattccga 1303  
 gataggatta tgcctagttt gtcatatcac agaaaaactc caagttaact tcatgttttg 1363  
 gaagggcagg tcgttttttaa agtatttcit tttttaactg gatgaaaaat cticattgta 1423  
 ggattaattt tcttaatcac ctccacacig tacagaggaa actcaagcct taaatgttta 1483  
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 accgcagggc ttgcctctgt caagtgtagc tctatctcag taattaaaat aagtgtgat 1603  
 ctactgattt tttttaatgg aticatttct aaatgggcat tataaataga gcttggttcat 1663  
 ttttaagaac gaaacattca taigataaac tatcgcttta aattgccttt ctggttcat 1723  
 ataacttttc cctgtcagga tccttagtgt ttgaaactcc tcgtgcgggg ctggcctcct 1783  
 gcggactcta gtttcgcctc ctgtagtggt cgccctggat ttcttcactt cagagctgta 1843  
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 caggaggcta aggtgggagg attcttagag cctgggaggt cgaggctgca gtgagctgtg 1963  
 attgtggcca ctgcactcca gcctgggtga cagagcgaga ctctgtctca aaaaagaaga 2023  
 aagagtaaga gctgaggcat ataatagaat tctgctaaag cacttaaggt gaaatcacat 2083  
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 ataaaatgta ctcattttca gtgtttttg 2172

<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro

1 5 10 15

Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr

20 25 30

Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys

35	40	45
Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys		
50	55	60
Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu		
65	70	75
Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser		
85	90	95
Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe		
100	105	110
Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg		
115	120	125
Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val		
130	135	140
Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu		
145	150	155
Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala		
165	170	

<210> 159

<211> 20

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 159

ggaagtgta ctctgctct

20

<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 160

gagagagaga gagagagaga actagtcctcg agtttttttt tttttttttt 50

<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt cccccccccc c 41

<210> 162

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence

<400> 162

agcaucgagu cggccuuguu ggccuacugg 30

<210> 163

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo (dT) primer sequence

<400> 163

gcggctgaag acggcctatg tggccttttt tttttttttt tt 42

<210> 164  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of the artificial sequence: an artificially synthesized primer  
 sequence  
 <400> 164  
 agcatcgagt cggccttggt g 21

<210> 165  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of the artificial sequence: an artificially synthesized primer  
 sequence  
 <400> 165  
 gcggctgaag acggcctatg t 21

<210> 166  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of the artificial sequence: an artificially synthesized primer  
 sequence  
 <400> 166  
 acittattgt catagtttag atctattttg 30

<210> 167  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of the artificial sequence: an artificially synthesized primer  
 sequence  
 <400> 167  
 ataatacctta aaaactccat ttccaccct 30

<210> 168  
 <211> 1536  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (139).. (1062)  
 <400> 168  
 GTGCTCCGCC GCCCGCCCCG ACCCGGGCCC AGCCGCCTCC ACGGCCCGCG CTCGTA CTGG 60  
 AGCGAAGAGC GGCTCCTGA GGGAGGGGAA GGGACGTGGG GGCGCCACG GCAGGATTAA 120  
 CCTCCATTTT AGCTAATC ATG GGA GAG ATT AAA GTC TCT CCT GAT TAT AAC 171  
 Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn  
 1 5 10



TGG TTT AGA GGT ACA GTT CCC CTT AAA AAG ATT ATT GTG GAT GAT GAT	219
Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp	
15 20 25	
GAC AGT AAG ATA TGG TCG CTC TAT GAC GCG GGC CCC CGA AGT ATC AGG	267
Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg	
30 35 40	
TGT CCT CTC ATA TTC CTG CCC CCT GTC AGT GGA ACT GCA GAT GTC TTT	315
Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe	
45 50 55	
TTC CGG CAG ATT TTG GCT CTG ACT GGA TGG GGT TAC CGG GTT ATC GCT	363
Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala	
60 65 70 75	
TTG CAG TAT CCA GTT TAT TGG GAC CAT CTC GAG TTC TGT GAT GGA TTC	411
Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe	
80 85 90	
AGA AAA CTT TTA GAC CAT TTA CAA TTG GAT AAA GTT CAT CTT TTT GGC	459
Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly	
95 100 105	
GCT TCT TTG GGA GGC TTT TTG GCC CAG AAA TTT GCT GAA TAT ACT CAC	507
Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His	
110 115 120	
AAA TCT CCT AGA GTC CAT TCC CTA ATC CTC TGC AAT TCC TTC AGT GAC	555
Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp	
125 130 135	
ACC TCT ATC TTC AAC CAA ACT TGG ACT GCA AAC AGC TTT TGG CTG ATG	603
Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met	
140 145 150 155	
CCT GCA TTT ATG CTC AAA AAA ATA GTT CTT GGA AAT TTT TCA TCT GGC	651
Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly	
160 165 170	
CCG GTG GAC CCT ATG ATG GCT GAT GCC ATT GAT TTC ATG GTA GAC AGG	699
Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg	
175 180 185	
CTA GAA AGT TTG GGT CAG AGT GAA CTG GCT TCA AGA CTT ACC TTG AAT	747
Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn	
190 195 200	
TGT CAA AAT TCT TAT GTG GTA CCT CAT AAA ATT CGG GAC ATA CCT GTA	795
Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val	
205 210 215	

ACT ATT ATG GAT GTG TTT GAT CAG AGT GCG CTT TCA ACT GAA GCT AAA	843
Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys	
220 225 230 235	
GAA GAA ATG TAC AAG CTG TAT CCT AAT GCC CGA AGA GCT CAT CTG AAA	891
Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys	
240 245 250	
ACA GGA GGC AAT TTC CCA TAC CTG TGC AGA AGT GCA GAG GTC AAT CTT	939
Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu	
255 260 265	
TAT GTA CAG ATA CAT TTG CTG CAA TTC CAT GGA ACC AAA TAC GCG GCC	987
Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala	
270 275 280	
ATT GAC CCA TCA ATG GTC AGT GCC GAG GAG CTT GAG GTG CAG AAA GGC	1035
Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly	
285 290 295	
AGC CTT GGC ATC AGC CAG GAG GAG CAG TAGTGTGTCT CTCGCTGTCA ATGATGA	1089
Ser Leu Gly Ile Ser Gln Glu Glu Gln	
300 305	
GTTGACCCGG TGTGTTCTTG TATAGTCAGT GGCATCAGCA CCCGTCAGCC GGCCTTTTCC	1149
TTCAGGTTTCG TCAGGCTCAC CGGTTCTCAC TGTGTCTGGG AAGTAGGACT GATGGTCATC	1209
TTCATGACAG GCGGCATCTC CACTAAGCCT GTGTAACGT TCCCTCTTTG GTTTTCTTAG	1269
CTTTTGAATT TGAAGAAGTA CTTTGAAGA CTCCCATTTT AAGAACCGTG CAGATTTTGC	1329
TACCAAAAGT CTTACCACT GTGTTCTTAA GTGAATGTA ATTTCTGAGG TTTGGGACTT	1389
TGTGGTGGTT TTTTCTTCT TTTCTTTTCC ATTCTTCTT CTTTCTTTT ATGTTGTTG	1449
CTGTAAATGC TGCACATCCA GATTGCATAT CAGGACATTG GTTATTTTAT GCTTCTTGG	1509
ATATAACCAT GATCAGAGTG CCATGGC	1536

<210> 169

<211> 308

<212> PRT

<213> Homo sapiens

<400> 169

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr	
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Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Ser Lys Ile Trp	
20 25 30	
Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe	
35 40 45	
Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu	
50 55 60	
Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val	
65 70 75 80	
Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp	
85 90 95	
His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly	
100 105 110	
Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val	

	115		120		125										
His	Ser	Leu	Ile	Leu	Cys	Asn	Ser	Phe	Ser	Asp	Thr	Ser	Ile	Phe	Asn
	130					135						140			
Gln	Thr	Trp	Thr	Ala	Asn	Ser	Phe	Trp	Leu	Met	Pro	Ala	Phe	Met	Leu
145					150					155					160
Lys	Lys	Ile	Val	Leu	Gly	Asn	Phe	Ser	Ser	Gly	Pro	Val	Asp	Pro	Met
			165						170					175	
Met	Ala	Asp	Ala	Ile	Asp	Phe	Met	Val	Asp	Arg	Leu	Glu	Ser	Leu	Gly
		180						185					190		
Gln	Ser	Glu	Leu	Ala	Ser	Arg	Leu	Thr	Leu	Asn	Cys	Gln	Asn	Ser	Tyr
	195					200					205				
Val	Val	Pro	His	Lys	Ile	Arg	Asp	Ile	Pro	Val	Thr	Ile	Met	Asp	Val
	210				215						220				
Phe	Asp	Gln	Ser	Ala	Leu	Ser	Thr	Glu	Ala	Lys	Glu	Glu	Met	Tyr	Lys
225					230					235					240
Leu	Tyr	Pro	Asn	Ala	Arg	Arg	Ala	His	Leu	Lys	Thr	Gly	Gly	Asn	Phe
			245					250						255	
Pro	Tyr	Leu	Cys	Arg	Ser	Ala	Glu	Val	Asn	Leu	Tyr	Val	Gln	Ile	His
		260					265						270		
Leu	Leu	Gln	Phe	His	Gly	Thr	Lys	Tyr	Ala	Ala	Ile	Asp	Pro	Ser	Met
	275					280						285			
Val	Ser	Ala	Glu	Glu	Leu	Glu	Val	Gln	Lys	Gly	Ser	Leu	Gly	Ile	Ser
	290					295					300				
Gln	Glu	Glu	Gln												
305															

<210> 170  
 <211> 2560  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 (202).. (1002)  
 <400> 170

CTGGCCTACT	GGGGCTCCAG	CCGTGTCCTG	AGGAGCTGGA	CCAGCCACAT	CCCCTGGGGC	60
TGCAGTTGAA	GCAGAACCAA	GTGGCCATCC	CGGCGTTAGA	CCGTAGGTTC	CTGGTCCCGG	120
AGTGGTCGGA	GCCCGCCAGT	GGGCAGGCAG	CTCTTGCTCA	CAGGCCGCGG	TGCCCAGGCC	180
GCTGGCTCTC	CGCAGGGCGG	A ATG GCG CTG CAA GTG	GAG CTG GTA CCC ACC			231
		Met Ala Leu Gln Val	Glu Leu Val Pro Thr			
		1	5		10	
GGG GAG ATC ATC CGC GTG GTT CAT CCC CAC AGG CCC TGC AAG CTT GCC		279				
Gly Glu Ile Ile Arg Val Val His Pro His Arg Pro Cys Lys Leu Ala						
	15	20	25			
CTG GGC AGT GAC GGG GTT CGG GTG ACC ATG GAG AGT GCG CTC ACC GCC		327				
Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala Leu Thr Ala						
	30	35	40			
CGT GAC CGG GTG GGG GTG CAG GAT TTC GTG CTG CTG GAG AAC TTC ACC		375				
Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr						
	45	50	55			

AGC GAG GCC GCC TTC ATC GGG AAC CTG CGG CGG CGA TTT CGG GAG AAT	423
Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn	
60 65 70	
CTC ATC TAC ACC TAC ATT GGC CCC GTC CTG GTC TCT GTC AAT CCC TAC	471
Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr	
75 80 85 90	
CGG GAC CTG CAG ATC TAC AGC CGG CAG CAT ATG GAG CGT TAC CGT GGC	519
Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly	
95 100 105	
GTC AGC TTC TAT GAA GTG CCC CCT CAC CTG TTT GCC GTG GCG GAC ACT	567
Val Ser Phe Tyr Glu Val Pro Pro His Leu Phe Ala Val Ala Asp Thr	
110 115 120	
GTG TAC CGA GCA CTG CGC ACG GAG CGT CGG GAC CAG GCT GTG ATG ATC	615
Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile	
125 130 135	
TCT GGG GAG AGC GGG GCA GGC AAG ACC GAG GCC ACC AAG AGG CTG CTG	663
Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu	
140 145 150	
CAG TTC TAT GCA GAG ACC TGC CCA GCC CCC GAG CGC GGA GGT GCC GTG	711
Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val	
155 160 165 170	
CGG GAC CGG CTG CTA CAG AGC AAC CCG GTG CTG GAG GCC TTT GGA AAT	759
Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn	
175 180 185	
GCC AAG ACC CTC CGG AAC GAT AAC TCC AGC AGG TTC GGG AAG TAC ATG	807
Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met	
190 195 200	
GAT GTG CAG TTT GAC TTC AAG GGT GCC CCC GTG GGT GGC CAC ATC CTC	855
Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu	
205 210 215	
AGT TAC CCC CTG GAA AAG TCA CGA GTG GTG CAC CAG AAT CAT GGG GAG	903
Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu	
220 225 230	
CGG AAC TTC ACA TCT TCT ACC AGC TGC TGG AGG GGG GCG AGG AGG AGA	951
Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg	
235 240 245 250	
CTC TTC GCA GGC TGG GCT TGG AAC GGA ACC CCC AGA GCT ATC TGT ACC	999
Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr	
255 260 265	
TGG TGAAGGCCAG TGTGCCAAAG TCTTCTTCAT CAACGACAAG AGTGACTGGA AGGTCG	1058

Trp

TCAGGAAGGC	TCTGACAGTC	ATTGATTTC	CCGAGGATGA	AGTGGAGGAC	CTGCTGAGCA	1118
TCGTGGCCAG	CGTCCTTCAT	TTGGGCAACA	TCCACTTTGC	TGCCAACGAG	GAGAGCAATG	1178
CCCAGGTCAC	CACCGAGAAC	CAGCTCAAGT	ATCTGAGCCC	ATTGAGTATG	CGGTGCCTGT	1238
TGTGAAATAC	GACCGCAAGG	GCTACAAGCC	TGCTCCCCTG	CAGCTGCTGC	TCACGCCCAA	1298
CGCCGTCTGC	ATCGTGGAGG	ACGCCAAAGT	CAAGCAGAGG	ATTGATTACG	CCAACCTGAC	1358
CGGAATCTCT	GTCAGCAGCC	TGAGCGACAG	TCTTTTGTG	CTTCATGTAC	AGCGTGCGGA	1418
CAATAAGCAA	AAGGGAGATG	TGGTGCTGCA	GAGTGACCAC	GTGATTGAGA	CGCTGACCAA	1478
GACAGCCCTC	AGTGCCAACC	GCGTGAACAG	CATCAACATC	AACCAGGGCA	GCATCACGTT	1538
TGCAGGGGGC	CCCGGCAGGG	ATGGCACCAT	TGACTTCACA	CCCGGCTCGG	AGCTGCTCAT	1598
CACCAAGGCC	AAGAACGGGC	ACCTGGCTGT	GGTCGCCCCA	CGGCTGAATT	CTCGGTGATA	1658
AAGGCGCCCA	CTGGACCCCT	CCAACGCCCA	ATGCTTTGCT	TTTCTCCTCC	TCCCCTTCCC	1718
AGTTACCAAA	GACTCGAACT	TCCAGACAGG	GACCCAGGGA	CACCCCGAAG	CCCACCTGCA	1778
ATCTCCCAAC	TCCTGCCCCT	CCCTCTCTTG	AGGGAGCAGC	AGGGGCCAGG	AGCTACCCCA	1838
GGAGTGGGCC	AGGCCGGGCC	ACAGCAATAG	GAAAGCCAGG	GCCAGAGCGA	GCCATGCCAG	1898
CCCTACTGCC	GATGCCAAAT	ATTTGAGAGA	AGGGAACTTT	TGCTGAGGTT	TTCTCTGAGG	1958
TTTTTTTTGA	TGCTTTATAG	GAAACTATTT	TTTAAAAAAA	GCCATTTCCC	ACCCAAGGAC	2018
ACAGTGGATG	TGTTTTCCCT	GACTCCAGCA	GGGCAAGGAA	ATGTAGCCGA	GAGGTTGTGT	2078
GGGTGGGGCT	CTGGTGCCCT	CTTCCCTGGC	CAGGACACCT	CTCCTCCTGA	TTCCCTTGGC	2138
ACCTTGCTTT	TCTGTCTGTT	TACCTGTCTC	CCTGCCTGCC	CATCTGCATC	TTTTGCAGCC	2198
CACTCTGACT	TCCATCTGGG	GGCTGAGACC	ACCCTTGCCCT	GCCCCCTTCT	TTCTGCCTTA	2258
AGAATGTCCT	TTTAGGCTGG	GCATGGTGGC	TCACGCCTGT	AACCCAGCA	CTTTGGGAGG	2318
CGGAGACGGG	CAGATAACCT	GAGGTCAGGA	TTTCGAGACC	AACCTGACCT	ACATGGAGAA	2378
ACTCCGCCTC	TGGTAAGGAT	ACAAAATTAG	CCGGGCATGG	TGGTGCACGC	CTCTAATCCC	2438
AGCTGCTCGG	GAGGCTGAGG	CAGGAGAATC	ACTTGAACCC	GGGAAGTGA	GGTTGCAGTG	2498
AGCCAAGAGT	ACACCACTGC	ACTCCAGCCT	GGGCAACAGA	GCGAGACTCC	GTCTTAAAAA	2558
AA						2560

<210> 171

<211> 267

<212> PRT

<213> Homo sapiens

<400> 171

Met	Ala	Leu	Gln	Val	Glu	Leu	Val	Pro	Thr	Gly	Glu	Ile	Ile	Arg	Val
1				5					10					15	
Val	His	Pro	His	Arg	Pro	Cys	Lys	Leu	Ala	Leu	Gly	Ser	Asp	Gly	Val
			20					25					30		
Arg	Val	Thr	Met	Glu	Ser	Ala	Leu	Thr	Ala	Arg	Asp	Arg	Val	Gly	Val
		35					40				45				
Gln	Asp	Phe	Val	Leu	Leu	Glu	Asn	Phe	Thr	Ser	Glu	Ala	Ala	Phe	Ile
	50				55					60					
Gly	Asn	Leu	Arg	Arg	Arg	Phe	Arg	Glu	Asn	Leu	Ile	Tyr	Thr	Tyr	Ile
	65			70				75						80	
Gly	Pro	Val	Leu	Val	Ser	Val	Asn	Pro	Tyr	Arg	Asp	Leu	Gln	Ile	Tyr
		85					90						95		
Ser	Arg	Gln	His	Met	Glu	Arg	Tyr	Arg	Gly	Val	Ser	Phe	Tyr	Glu	Val
		100					105					110			
Pro	Pro	His	Leu	Phe	Ala	Val	Ala	Asp	Thr	Val	Tyr	Arg	Ala	Leu	Arg
		115				120						125			
Thr	Glu	Arg	Arg	Asp	Gln	Ala	Val	Met	Ile	Ser	Gly	Glu	Ser	Gly	Ala
	130				135					140					
Gly	Lys	Thr	Glu	Ala	Thr	Lys	Arg	Leu	Leu	Gln	Phe	Tyr	Ala	Glu	Thr

145		150		155		160									
Cys	Pro	Ala	Pro	Glu	Arg	Gly	Gly	Ala	Val	Arg	Asp	Arg	Leu	Leu	Gln
		165		170		175									
Ser	Asn	Pro	Val	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Leu	Arg	Asn
		180		185		190									
Asp	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Tyr	Met	Asp	Val	Gln	Phe	Asp	Phe
		195		200		205									
Lys	Gly	Ala	Pro	Val	Gly	Gly	His	Ile	Leu	Ser	Tyr	Pro	Leu	Glu	Lys
		210		215		220									
Ser	Arg	Val	Val	His	Gln	Asn	His	Gly	Glu	Arg	Asn	Phe	Thr	Ser	Ser
		225		230		235									
Thr	Ser	Cys	Trp	Arg	Gly	Ala	Arg	Arg	Arg	Leu	Phe	Ala	Gly	Trp	Ala
				245				250						255	
Trp	Asn	Gly	Thr	Pro	Arg	Ala	Ile	Cys	Thr	Trp					
			260					265							

<210> 172  
 <211> 2650  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (116).. (1216)  
 <400> 172

CTTTTGCTGC	TGCGCCCGGG	CAGGGGCTGC	CGCGGCCCCA	GGTCCCGCTT	CGAGACGCGG	60
CGCGGTCCAG	GCGGGAGGCG	ACTCCCTAGG	AAGGGACCCG	GGGCGGGAGG	AGGAA ATG	118
					Met	
					1	
AGG CCG CGC GGA AGG AAG GCG GCG AGC CCC GGG GCC CCG AGG CCT TGG						166
Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp						
	5		10		15	
CCG CGT CAC AGC ACC CAC ATG GCC TCT GGA GTG GGC GCG GCC TTC GAG						214
Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu						
	20		25		30	
GAA CTG CCT CAC GAC GGC ACG TGT GAC GAG TGC GAG CCC GAC GAG GCT						262
Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala						
	35		40		45	
CCG GGG GCC GAG GAA GTG TGC CGA GAA TGC GGC TTC TGC TAC TGC CGC						310
Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg						
	50		55		60	65
CGC CAT GCC GAG GCG CAC AGG CAG AAG TTC CTC AGT CAC CAT CTG GCC						358
Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala						
	70		75		80	
GAA TAC GTC CAC GGC TCC CAG GCC TGG ACC CCG CCA GCT GAC GGA GAG						406
Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu						
	85		90		95	

GGG GCG GGG AAG GAA GAA GCG GAG GTC AAG GTG GAG CAG GAG AGG GAG Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu 100 105 110	454
ATA GAA AGC GAG GCA GGG GAA GAG AGT GAG TCG GAG GAA GAG AGC GAG Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu 115 120 125	502
TCA GAG GAA GAG AGC GAG ACA GAG GAA GAG AGT GAG GAT GAG AGC GAT Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp 130 135 140 145	550
GAG GAG AGT GAA GAA GAC AGC GAG GAA GAA ATG GAG GAT GAG CAA GAA Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu 150 155 160	598
AGC GAG GCC GAA GAA GAC AAC CAA GAA GAA GGG GAA TCC GAG GCG GAG Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu 165 170 175	646
GGA GAA ACT GAG GCA GAA AGT GAA TTT GAC CCA GAA ATA GAA ATG GAA Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu 180 185 190	694
GCA GAG AGA GTG GCC AAG AGG AAG TGT CCG GAC CAT GGG CTT GAT TTG Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu 195 200 205	742
AGT ACC TAT TGC CAG GAA GAT AGG CAG CTC ATC TGT GTC CTG TGT CCA Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro 210 215 220 225	790
GTC ATT GGG GCT CAC CAG GGC CAC CAA CTC TCC ACC CTA GAC GAA GCC Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala 230 235 240	838
TTT GAA GAA TTA AGA AGC AAA GAC TCA GGT GGA CTG AAG GCC GCT ATG Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met 245 250 255	886
ATC GAA TTG GTG GAA AGG TTG AAG TTC AAG AGC TCA GAC CCT AAA GTA Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val 260 265 270	934
ACT CGG GAC CAA ATG AAG ATG TTT ATA CAG CAG GAA TTT AAG AAA GTT Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val 275 280 285	982
CAG AAA GTG ATT GCT GAT GAG GAG CAG AAG GCC CTT CAT CTA GTG GAC Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp 290 295 300 305	1030
ATC CAA GAG GCA ATG GCC ACA GCT CAT GTG ACT GAG ATA CTG GCA GAC	1078

Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala	Asp	
				310					315					320		
ATC	CAA	TCC	CAC	ATG	GAT	AGG	TTG	ATG	ACT	CAG	ATG	GCC	CAA	GCC	AAG	1126
Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala	Lys	
			325					330					335			
GAA	CAA	CTT	GAT	ACC	TCT	AAT	GAA	TCA	GCT	GAG	CCA	AAG	GCA	GAG	GGC	1174
Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu	Gly	
		340					345					350				
GAT	GAG	GAA	GGA	CCC	AGT	GGT	GCC	AGT	GAA	GAA	GAG	GAC	ACA	TGAAGGCTT		1225
Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr			
	355					360					365					
GCTACCCCCA	GTGGAAAATC	ATCCCCTCCC	CTTGTGTGTA	TGTGACAGCG	TGTATGTAAC											1285
GGCTTCTGAT	TTCTGTGAAA	GCTGCTCAGC	AACAAACGTA	CTTCCACCAG	ATGTGTCCCC											1345
AGATCCACAG	CAGGCACATA	TCTCTCCAAG	GGATGACCAG	TTTTATGCTT	ACTGTGTGCT											1405
TCTCATCCCC	TGGTTGTGGT	AGGTCAAGGA	AAAGAGCCCC	TTTGATCCAC	CAGGAGCAAT											1465
TAAGAAAGGT	CCTTCAGGTA	ATCCCTCAAT	GGCTGCTTTG	AACTTACTCA	GGAAAGCCAG											1525
CCCCCATAAT	ATTGTATTAC	CAAAACAGTAT	CGCTTTGTTA	GGAAGGATCT	GGAATAATCT											1585
TGAAGGGAAG	TCAGAGTTTT	CTCCCTGCCT	ATTAACAAAA	ACCCAATTTT	GTTCATATTG											1645
AAGCATGAAA	TAAATGAGAG	CAAGGTAGGG	CCAAATTAAC	TCTTGTGGAC	AGTCCCTAAA											1705
AGTCCAGTTC	TACATTTGTG	AAAATTGTGG	TGCCATGAAT	TAAGATGGAT	GA CTGGAAAA											1765
AGGTGTTGGA	GAAAGAGTTA	AAGATGAGGA	AGAGATATTT	TTAGTATATG	AAGTTATCCA											1825
GGACTTGATA	TTCATAATTC	AGTGCTGTGG	AAATGAAAAA	AATGATTGAA	GAGGTGGAAC											1885
GGAAATGACC	TTAGGGGGAA	AAAAAAGGAC	CAAAGAAGTC	TGATTAAAAG	TTGAAATCAG											1945
TATTTCTGAA	TTCAAATTGC	TTGAATTTCC	AAAATAGTCA	GTAAAGGATC	TAATAGAACC											2005
AGAATTATTT	GGGTGAATTC	TGCAGGTTTT	ATGGGCTTGT	CACAACGTGA	AGGGCTGGAA											2065
TGTATATTAC	CAAATGGGAA	TTTCCATTGT	AGGTTTTTGC	TAGTCCCACC	CCCATTTTAG											2125
CCTAATTTGG	CTTAAACGCA	GTATGGGGAG	AATTGTTCCC	ATTCCATGTG	TTCTGAATTC											2185
AGCTCATCTC	CCAGCATATA	GATATATCCT	CCTTTAACTC	CGACCAGAAC	CCTTCTTCCT											2245
GTGGCACTCC	CCACCCATAG	ACCTTCAGAT	CATCTCCAC	ACCCTGGATC	TCACTCTCCT											2305
CTTAGTAACA	GAGACACTCC	TGAGGTTGGA	CTTCCTTGCT	TTTCTCTACT	TCCAAATCAC											2365
AATTTCTTAC	AACCAAGCTT	TGTGCTCCCG	AGTAAGCAGG	GATGTACTAG	GGGAATGTAA											2425
AACTGCAAAC	TTAAAAACCT	GCATCTTCTT	GAAGCATCAG	TTTTACTTAC	CAAATGGTTT											2485
AGAGTCATAA	GATGACCTAT	TTTTATATAA	AAGTTATATT	ATAGAATAAA	ATGTTCATAC											2545
GCATAGACTG	TTAAG															2560

<210> 173

<211> 367

<212> PRT

<213> Homo sapiens

173

Met	Arg	Pro	Arg	Gly	Arg	Lys	Ala	Ala	Ser	Pro	Gly	Ala	Pro	Arg	Pro	
1				5					10					15		
Trp	Pro	Arg	His	Ser	Thr	His	Met	Ala	Ser	Gly	Val	Gly	Ala	Ala	Phe	
			20					25					30			
Glu	Glu	Leu	Pro	His	Asp	Gly	Thr	Cys	Asp	Glu	Cys	Glu	Pro	Asp	Glu	
		35				40						45				
Ala	Pro	Gly	Ala	Glu	Glu	Val	Cys	Arg	Glu	Cys	Gly	Phe	Cys	Tyr	Cys	
	50					55					60					
Arg	Arg	His	Ala	Glu	Ala	His	Arg	Gln	Lys	Phe	Leu	Ser	His	His	Leu	



65					70					75					80
Ala	Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly
				85					90					95	
Glu	Gly	Ala	Gly	Lys	Glu	Glu	Ala	Glu	Val	Lys	Val	Glu	Gln	Glu	Arg
			100					105					110		
Glu	Ile	Glu	Ser	Glu	Ala	Gly	Glu	Glu	Ser	Glu	Ser	Glu	Glu	Glu	Ser
		115					120					125			
Glu	Ser	Glu	Glu	Glu	Ser	Glu	Thr	Glu	Glu	Glu	Ser	Glu	Asp	Glu	Ser
	130					135					140				
Asp	Glu	Glu	Ser	Glu	Glu	Asp	Ser	Glu	Glu	Glu	Met	Glu	Asp	Glu	Gln
145					150					155					160
Glu	Ser	Glu	Ala	Glu	Glu	Asp	Asn	Gln	Glu	Gly	Glu	Ser	Glu	Glu	Ala
			165					170					175		
Glu	Gly	Glu	Thr	Glu	Ala	Glu	Ser	Glu	Phe	Asp	Pro	Glu	Ile	Glu	Met
		180						185				190			
Glu	Ala	Glu	Arg	Val	Ala	Lys	Arg	Lys	Cys	Pro	Asp	His	Gly	Leu	Asp
	195						200					205			
Leu	Ser	Thr	Tyr	Cys	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys
	210					215					220				
Pro	Val	Ile	Gly	Ala	His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu
225					230					235					240
Ala	Phe	Glu	Glu	Leu	Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala
			245					250						255	
Met	Ile	Glu	Leu	Val	Glu	Arg	Leu	Lys	Phe	Lys	Ser	Ser	Asp	Pro	Lys
		260						265					270		
Val	Thr	Arg	Asp	Gln	Met	Lys	Met	Phe	Ile	Gln	Gln	Glu	Phe	Lys	Lys
		275					280					285			
Val	Gln	Lys	Val	Ile	Ala	Asp	Glu	Glu	Gln	Lys	Ala	Leu	His	Leu	Val
	290					295					300				
Asp	Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala
305					310					315					320
Asp	Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala
				325						330					335
Lys	Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu
			340					345						350	
Gly	Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr	
		355					360					365			

<210> 174

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 174

ttaagccttgc caccatgagc aaccccagcg ccccaccacc a

41

<210> 175

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 175

gtatcgattt aattgcgatc ccccatcag

29

176

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 176

cacctactgtatgacaccacattc

24

<210> 177

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 177

gagatgcigtccatgctggcctg

24

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 178

ggaaagcctcctcgctggctaacaag

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 179

catagtccttgacaagggtcacag

24

<210> 180

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 180

cccatcaccatcttccaggagc

22

<210> 181

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 181

ttcaccaccttcttgatgcatcata

26